

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 17:37:52 ; Search time 2932.86 Seconds
(without alignments)
5458.535 Million cell updates/sec

Title: US-09-601-138-1
Perfect score: 1035
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 773874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1035	100.0	1113	9	AX079028
5	1035	100.0	1260	9	AX020191
6	1035	100.0	1260	10	AX079037
7	1035	100.0	3988	9	AX020190
8	1035	100.0	3988	10	AX079036

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10	1033.4	99.8	1035	9	AX020184	AX020184 Sequence
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15	1030.2	99.5	1035	9	AX020189	AX020189 Sequence
16	1030.2	99.5	1035	10	AX079035	AX079035 Sequence
17	1030.2	99.5	1035	10	AX079035	AX079035 Sequence
18	1030.2	99.5	5445	9	AX020192	AX020192 Sequence
19	1028.6	99.4	1035	9	AX020186	AX020186 Sequence
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25	1021.4	98.7	1034	9	AX020188	AX020188 Sequence
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ALIGNMENTS

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LOCUS AX020182 1035 bp DNA
DEFINITION Sequence 1 from Patent WO937325.
ACCESSION AX020182
VERSION AX020182.1 GI:10043973
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Fogh, J. and Gellerfors, P.
TITLE Method for treating acute intermittent porphyria (aip) and other
JOURNAL porphyric diseases
Patent: WO 93/7325-A1 29-JUL-1993;
FOCH JENS (DK); HEMPHOTEC A S (DK); GELLERFORS PAER (SE)
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source location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 250 a 271 c 302 g 212 t
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Query Match 100.0%; Score 1035; DB 9; Length 1035;
Best Local Similarity 100.0%; Pred. No. 4.5e-238;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
LOCUS AX079027 1035 bp DNA PAT 22-FEB-2001

DEFINITION Sequence 3 from Patent WO0107065.
ACCESSION AX079027
VERSION AX079027.1 GI:13158602
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1035)
TITLE Gellierfors, P. and Fogh, J.
Production of rhbpgd and new therapeutic methods for treating
patients with acute intermittent porphyria (aip) and other
porphyric diseases
Patent: WO 0107065-A 3 01-FEB-2001;
JOURNAL HemeBioTech A/S (DK)
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source Location/Qualifiers
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/organism="Homo sapiens"
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Query Match 100.0%; Score 1035; DB 10; Length 1035;
Best Local Similarity 100.0%; Pred. No. 4.5e-238;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX020193
DEFINITION Sequence 12 from Patent WO937325.
ACCESSION AX020193
VERSION AX020193.1 GI:10043984
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1113)
AUTHORS Fogh, J. and Gellierfors, P.
TITLE Method for treating acute intermittent porphyria (aip) and other
porphyric diseases
Patent: WO 937325-A 12 29-JUL-1999;
JOURNAL FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLIERFORS PAER (SE)
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Query Match 100.0%; Score 1035; DB 9; Length 1113;
Best Local Similarity 100.0%; Pred. No. 4.5e-238;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX079028 1113 bp DNA
DEFINITION Sequence 4 from Patent WO0107065.
ACCESSION AX079028
VERSION AX079028.1 GI:13158603
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Muller, P. and Fogh, J.
TITLE Production of rHbpd and new therapeutic methods for treating
 patients with acute intermittent porphyria (aip) and other
 porphyric diseases
JOURNAL Patent: WO 0107065-A 4 01-FEB-2001;
 Hemediotech A/S (DK)

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LOCUS AX020191 Sequence 10 from Patent WO937325.
DEFINITION AX020191
ACCESSION AX020191 GI:10043982
VERSION
KEYWORDS
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REFERENCE 1 (bases 1 to 1260)
AUTHORS Fogh,J. and Gellerafors,P.
TITLE Method for treating acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 937325-A 10 29-JUL-1999;
FOGH JENS (DK); HEMEDIOTECH A S (DK); GELLERFORS PAER (SE)
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Query Match 100.0%; Score 1035; DB 9; Length 1260;
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ACCESSION AX079037
VERSION AX079037.1 GI:13158612
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Gellerafors,P. and Fogh,J.
TITLE Production of rhbgd and new therapeutic methods for treating
patients with acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 0107065-A 13 01-FEB-2001;
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DEFINITION Sequence 9 from Patent WO9937325.
ACCESSION AX020190
VERSION AX020190.1 GI:10043981
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT 918 a 1056 c 1000 g 1014 t
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Query Match 100.0%; Score 1035; DB 9; Length 3988;
Best Local Similarity 100.0%; Pred. No. 3,7e-238;
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1 (bases 1 to 3988)				
Gallieriors, P. and Fogh, J.				
Production of rhpbgd and new therapeutic methods for treating				
patients with acute intermittent porphyria (aip) and other				
porphyric diseases				
Patent: WO 0107065-A				
12 01-FEB-2001;				
Hembiotech A/S (DK)				

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SOURCE	unidentified.			
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REFERENCE	1 (bases 1 to 1035)			
AUTHORS	Fogh, J. and Gellerfors, P.			
TITLE	Method for treating acute intermittent porphyria (aip) and other porphyric diseases			
JOURNAL	Patent: WO 93/37325-A 2 29-JUL-1999.			
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DEFINITION Sequence 3 from Patent WO937325.
ACCESSION AX020184
VERSION AX020184.1 GI:10043975
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SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1035)
AUTHORS Fogh,J. and Gellerfors,P.
TITLE Method for treating acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 937325-A 3 29-JUL-1999;
FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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QY	661	ctgcacgatacccggaagactctgctctgccttgatcgcgttgaaaggcccttccttgaaagcactg	720
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LOCUS	AX079029
DEFINITION	AX079029 Sequence 5 from Patent WO0107065.
ACCESSION	AX079029
VERSION	AX079029.1
KEYWORDS	GI:13158604
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 1035)
TITLE	Gellerfors, P. and Fogh, J.
JOURNAL	Production of rhpbgd and new therapeutic methods for treating porphyric diseases
FEATURES	Patent: WO 0107065-A 5 01-FEB-2001;
SOURCE	Hemebiotech A/S (DK)
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BASE COUNT	250 a 271 c 303 g 211 t
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Best Local Similarity	99.8%	Pred. NO. 1.1e-237					
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Db	1 ATGAAGAAGTATTCCGCTGGGTACCCGCACAGACCCACCTCTCGCTACGACAGGAGCACT	60					
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Db	121	ACCACAGGGGACAAAGATCTTGTATCTACTGCACCTCTTAAGATTTGAGAGAAAGCCGTGTTT	180
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Qy	421	ttcccgcatcttgagttcagagatltcggggaaactcaaacccgggcttctggaagctg	480
Db	421	TTCCCGCATCTGTGAGTTCAAGAGATATTCCGGGAAACCTCAACACCCTGGCTTCGGAACCTG	480
Qy	481	gagcagaagaagaagtctcagttgcatacactcgtggaagaagaagtcggccctgtgcaagcagatggc	540
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Qy	841	accalccatgltccctgtgccagcaatgaagaatggccccctgtgagatltgaaccaagltgttagtc	900
Db	841	ACCATTCATGTCCCTGCCCGCATGAAGATGGCCCTGTAGAGATGACCCCACTTGGTGGGC	900
Qy	901	atcacatgtcgttaacatcttcacagaaggccccagtttgtgtctgcccagaactttggatagac	960
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Qy	1021	aaagatgccatttaa	1035
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DEFINITION	Sequence 6 from Patent WO0107065.
ACCESSION	AX079030

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VERSION      AX079030.1  GI:13158605
KEYWORDS
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ORGANISM      human.
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REFERENCE     Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
               1 (bases 1 to 1035)
               Gellerfors, P. and Fogh, J.
               Production of rhpbgd and new therapeutic methods for treating
               patients with acute intermittent porphyria (aip) and other
               porphyric diseases
               Patent: WO 0107065-A 6 01-FEB-2001;
JOURNAL      HemeBioTech A/S (DK)
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BASE COUNT   250 a      271 c      303 g      211 t
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Query Match          99.8%; Score 1033.4; DB 10; Length 1035;
Best Local Similarity 99.9%; Pred. No. 1.1e-237;
Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 421 ttcccgcaatctgaggttcaagagatctcggggaaacacacacacacacacacacacac 480
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ACCESSION     AX020187
VERSION       AX020187.1  GI:10043978
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SOURCE        unidentified.
               unclassified.
ORGANISM      unidentified.
REFERENCE     1 (bases 1 to 1035)
AUTHORS       Fogh, J. and Gellerfors, P.
TITLE         Method for treating acute intermittent porphyria (aip) and other
               porphyric diseases
JOURNAL       POGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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Best Local Similarity 99.8%; Pred. No. 2.7e-237;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION Sequence 9 from Patent WO0107065.
ACCESSION AX079033
VERSION AX079033.1 GI:13158608
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REFERENCE
  1 (bases 1 to 1035)
AUTHORS Gellerfors, P. and Fogh, J.
TITLE Production of rhbpd and new therapeutic methods for treating
  patients with acute intermittent porphyria (aip) and other
  porphyric diseases
JOURNAL Patent: WO 0107065-A 9 01-FEB-2001.
FEATURES
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BASE COUNT 250 a 270 c 303 g 212 t
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Query Match 99.7%: Score 1031.8; DB 10; Length 1035;
Best Local Similarity 99.8%: Pred. No. 2.7e-237;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 atgagagatgattcgtctgtggtlaacccgcaagagccagctgtctgcatacagaagcagct 60
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DEFINITION AX020189
ACCESSION AX020189
VERSION AX020189.1 GI:10043980
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1035)
AUTHORS Fogh, J. and Gellerfors, P.
TITLE Method for treating acute intermittent porphyria (aip) and other
JOURNAL porphyric diseases
FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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SOURCE location/Qualifiers
1. 1035
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BASE COUNT 251 a 272 c 302 g 210 t
ORIGIN

Query Match 99.5% Score 1030.2; DB 9; Length 1035;
Best Local Similarity 99.7% Pred. No. 6,4e-237;
Matches 1032; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 atggagtgatctgcggtgggtacccgcaagagccagctgtctgcatacagaagcaagt 60
Db 1 ATGAGAGGATTCGGTGGGTACCCGCAAGAGCCAGCTTGCTCCATACACAGCAGAGT 60
QY 61 gtggtagcaacatgtaaaacctcgtaacctgtgctgcaattgtgaatcatgtatgtcc 120
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QY 121 acccaaggagcaagatctctgtacatgacctctctaagalttgagaagaaagcctgtt 180
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Db 181 ACCAAGAGAGCTTGAACATGCCCTGAGAAAGATGAAGTGGACCTGGTTGTTCACTCTTG 240
QY 241 aaggacctgcccactgtgtctctcctgtgtccatcagaaatcgtgaaagcagagaa 300
Db 241 AAGGACCTGCCCACTGTGCTCTCTGCTTCCATCGAGCCATCTGCAAGCGGAA 300
QY 301 aaccctcatgtgtgtgtcttttcaaccacaattgtgtggaagaccttagaaacctg 360
Db 301 AACCTCATGTGTGTGTCTTTCAACCAAAATTTGTTGGGAAAGACCTTAGAAACCTTG 360
QY 361 ccagaaagagctgtgtgtggaacacagctccctgcaagagcagccagctgcaagaaag 420
Db 361 CCAGAGAAAGTGTGTGTGGGGAACACAGCTCCCTGCAAGAGACAGCCAGCTGCAGAGAAAG 420
QY 421 ttcccgcatctgtgagttcaggagatattcgggaaacctcaacacccggcttcggaagt 480
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QY 481 gacgagcagcagagagttcagttgcatcatcctgtgcaacagctgtgctgtcagcgcatggc 540
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QY 541 tggcacaaccgggttggcgagatccctgcaccccttgaggatgtatgtatgtgtgtggccag 600
Db 541 TGGCACAACCGGGTGGCGAGATCCCTGCACCCCTGAGGAATGATGTATGTGTGGCCAG 600
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Db 601 GGGGACCTTGGCGGTGGAAGTGCAGACCAAGGACAGACATCTTGTGATCTGTGTGTGTG 660
QY 661 ctgacagatcccgagaaacctgtctgtgcatgctgtgaaaggacctccctgaagcactg 720
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Db 841 ACCATCATGTCCCTACCCACCATGAGATGGCCCTGAGATGACCCACAGTTGTGTAGGC 900
QY 901 atcactgtctgaacatccacagagggccagctgtgctgtgccagaaacttgtagcagc 960
Db 901 ATCACTGCTGTAACTTCCACAGAGGCCCAAGTTGGCTGCCAGAACTTGGCATCAGC 960
QY 961 ctggccaactgtgtgtggaagaaagagcnaaaacacatcctgtgattgtgcagcgcaattg 1020
Db 961 CTGGCCAACCTGTGTGTGAGCAAGAGCCNAAAACATCTGTGATTGTGCAGCGCAATTG 1020
QY 1021 aacgaltgccattaa 1035
Db 1021 AACGATGCCATTAA 1035
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Search completed: October 6, 2001, 18:32:02
Job time: 3250 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 17:37:52 ; Search time 1970.35 seconds
(without alignments)
4965.465 Million cell updates/sec

Title: US-09-601-138-1
Perfect score: 1035
Sequence: 1 atgagagtgatctgcgtgg9.....aattgaacgatgcccattaa 1035

Scoring table: IDENTITY_NNC
Gapop 10.0 , Gapext 1.0

Searched: 1022815 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	837.4	80.9	882	105	AL524270
2	804.8	77.8	1036	105	AL524270
3	728.4	70.4	904	152	AL520285
4	711.4	68.7	949	106	BG337601
5	698.2	67.5	878	105	AL561865
6	690.4	66.7	942	106	AL561865
7	682	65.9	938	106	AL561865
8	671.4	64.9	904	137	AL561865
9	659.2	63.7	919	105	AL561865
10	650.4	62.8	801	143	AL561865
11	649.2	62.7	1136	137	AL561865
12	646.4	62.5	835	154	AL561865
13	635.6	61.4	908	105	AL561865
14	628.8	60.8	941	106	AL561865
15	610.2	59.0	812	108	AL561865
16	602.2	58.2	746	106	AL561865
17	586	56.6	695	136	AL561865
18	579.8	56.0	1087	137	AL561865
19	573	55.4	970	137	AL561865
20	568.2	54.9	883	107	AL561865
21	557	53.8	755	105	AL561865
22	549.4	53.1	693	140	AL561865
23	548	52.9	869	141	AL561865
24	544.8	52.6	840	141	AL561865
25	543	52.5	847	153	AL561865
26	539.8	52.2	795	141	AL561865
27	522.8	50.5	538	172	AL561865
28	513.2	49.8	807	108	AL561865
29	509	49.2	963	174	AL561865
30	506	48.9	766	167	AL561865
31	502.8	48.6	776	152	AL561865
32	491.4	47.5	873	152	AL561865
33	490.8	47.4	1090	175	AL561865
34	487.4	47.1	619	119	AL561865
35	485.8	46.9	807	107	AL561865
36	484.2	46.8	826	146	AL561865
37	483.8	46.7	1087	152	AL561865
38	482.2	46.6	1044	139	AL561865
39	479.4	46.3	849	152	AL561865
40	474.6	45.9	648	106	AL561865
41	472	45.6	655	190	AL561865
42	464	44.8	893	137	AL561865
43	458.6	44.3	741	107	AL561865
44	453.4	43.8	968	141	AL561865
45	450.8	43.6	797	15	AL561865

ALIGNMENTS

RESULT	1	AL524270	882 bp	mrna	EST	13-FEB-2001
LOCUS	AL524270	LRI_NFL003_NBC3	Homo sapiens	cdna	clone CS0DC002J01	5
DEFINITION	AL524270	prime, mRNA sequence.				
ACCESSION	AL524270					
VERSION	AL524270.1	GI:12787763				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	Li, W. B., Gruber, C., Jessee, J. and Polyes, D.					
TITLE	Full-length cDNA libraries and normalization					
JOURNAL	Unpublished (2001)					
COMMENT	Contact: Genoscope					

Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr.
Location/Qualifiers

FEATURES
source

1. 882
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC002J01"
/clone.lib="LRI_NFL003_NBC3"
/sex="male"
/tissue="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@life.com URL : http://fulllength.invitrogen.com"

BASE COUNT 205 a 236 c 262 g 178 t 1 others
ORIGIN

Query Match 80.9%; Score 837.4; DB 105; Length 882;
Best Local Similarity 99.2%; Pred. No. 3.4e-213;
Matches 882; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Oy	175	ctctttcaagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	234
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Oy	235	tccttgaagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	294
Db	61	tccttgaagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	120
Oy	295	cgggaagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	354
Db	121	cgggaagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	180
Oy	355	acccttgaagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	414
Db	181	acccttgaagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	240
Oy	415	agaagagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	474
Db	241	agaagagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	300
Oy	475	aagcttgaagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	534
Db	301	aagcttgaagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	360
Oy	535	atgagcttgaagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	594
Db	361	atgagcttgaagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	420
Oy	595	ggcagagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	654
Db	421	ggcagagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	480
Oy	655	ggtgtgttgaagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	714
Db	481	ggtgtgttgaagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	540
Oy	715	caacttgaagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	774
Db	541	caacttgaagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	599
Oy	775	ctgtacttgaagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	834
Db	600	ctgtacttgaagagagagcttgaacatgcccgggaagaatgaatgagctgtgtgttcac	659

QY	121	acacacaggggagacaaaggtctctctgtatctgacatctctcaaga	cttggaagagaaacccggtc	180
Db	299	ACCAACAAGGAGACAAAGATTCTTGTAAGTACTGGCACTCTCTAAGATTGGAAAGAA	AAACCCGCTGTTT	358
QY	181	accacgaagagcttgaacacatgcctctgnaaagaa	lgaagctggaacctgtcttcaactctgt	240
Db	359	ACCAAGAGAGCTTGAACATGCGCCCTGGAGAAAGAA	TGAAGTGAGACTGGTGTGTACCTCTTG	418
QY	241	aaggaacctgcccacctgtgtctctctctctgtgcttaccata	tggggaccatctgcgaacgggaa	300
Db	419	AAGGACTCTGCCACTGTGCTTCTCTCTCTGCTGTTCACCATG	GGAGGCCATCTGCAAGCCGGGAA	478
QY	301	aacctcatgatgtctgtctcttccaccccaaaatctgtcttgg	gaagaccttaagaacacctgt	360
Db	479	AAACCCATCATGATGCTGCTGTTCTTCTTCCACCAAAAT	TGTTGGGAGAACCTTAGMAACCTGT	538
QY	361	ccagaaagaagatgtgtgtgtggaaacccgctccctcg	cgaaagcagccagctctcaagagaag	420
Db	539	CCAGAGAAAGATGTGCTGGGAAACCAAGCTCCCTGCG	AAAGACAGCCAGCTGCAAGAAAG	598
QY	421	ttcccgcatctgtaggtctcagagataltcggggaa	aaacctcaaacaccgagcttcggaagtgt	480
Db	599	TTTCCCGCATCTGTGAGATTCTGAGAGTATTCGGGG	AAACCTCAACCCGGGTTTGGAAGCTGT	658
QY	481	gacgaagcaagagagatctagtgacatcatcctctg	gaaacagctctgagctctgaacgtcatgtggc	540
Db	659	GACGAGACACAGAGAGATTCTAGTGTCCATCATCT	GTGGCAACAGTGTGCTGTGACGACATGGGC	718
QY	541	tggcacaacacggagcttggggacagatctctgtca	ccctctggagaaatgcatgtatctgtggcgccag	600
Db	719	TGGCACAAACCGCGGTGGGGAGATCTCTGCA	CCCTGAGAGAAATGCATGTATCTGTGGCGCCAG	778
QY	601	ggggaccttggggcgttggaaagtgcgaaccca	aaaggacacggagcatcttgatctgtgtgggtgtgt	660
Db	779	GGGGCCTTGCGCGCTGGAAAGTGCAGACCCAA	AGAACAGCAAGCAATCTTGATCTGGTGGCTGTGT	838
QY	661	ctgcacagatcccgagacatctgtctgtcgtgtg	catctgcgtctgaagggacctctctgaagcactgt	720
Db	839	CTGCACAGATCTCCGAAACACTCTCTTGCTGTG	CAATCGCTGAAAGGGCCTTCTGTGAGGCA -CTG	897
QY	721	gaaggaagcctgagagtgctccagtgacgctgtga	ctataagctatgaagatagggcaactgtctac	780
Db	898	GAAAGAGAGCTGCAGTGTCTCCAGTACCCGTG	CAATACAGCTATGAAAGGAATGGGCAACTGTGAC	957
QY	781	ctgaacttgaaggaagtccttgagctctaga	acgctcaagaatgacatacaagagaacatcagagct	840
Db	958	CTGACTGTGAGAGAGTGTGAGGTCTAGAC -G	STGCAGATAGCAATTCAAAGACA -CATG	1015
QY	841	aacatcccatctgtccctgcgc	858	
Db	1016	A-CATTCATGTGTCCGCCCC	1032	

REFERENCE AUTHORS TITLE JOURNAL	ORGANISM	SEQUENCE SOURCE	KEYWORDS EST.
		human.	
		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
		1 (bases 1 to 904)	
		NIH-MGC http://mgc.ncl.nih.gov/	
		National Institutes of Health, Mammalian Gene Collection (MGC)	
		Unpublished (1999)	
		Contact: Robert Strausberg, Ph.D.	
		Email: cgaps-remail.nih.gov	
		Tissue Procurement: ATCC	
		CDNA Library Preparation: Ling Hong/Rubin Laboratory	

The normalized libraries library was constructed by Life Technologies. Contact : Feng Liang life technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com>

Query Match 67.5%; Score 698.2; DB 105; Length 878;
Best Local Similarity 94.3%; Pred. NO. 5.6e-176;
Matches 746; Conservative 4; Mismatches 2; Indels 39; Gaps 1;

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QY	96	gcagcttgaatactatgcatagtccaccacagaggacagaattcttatactgacctc	155
Db	187	gcactttgaaatcattgtctatgtccacacacagggacaaagattttgatctgacacttc	246
QY	156	taagatttgagagaagaagccctggtttaccagaaggagcttgaacaatgccttgagaagaatga	215
Db	247	ttaaatgttgagagagaaaaagccctgttttaccagaagaccttgaacatgacccctcgagaaagatga	306
QY	216	agtgagaccctggttctcaactccttgaagagaccctgacacatgtgcttcctctggtctaac	275
Db	307	agtgagaccctggttctcaactccttgaagagacacctccacactgtgcttcctctggtctaac	366
QY	276	catcgagagccatctgcacaagcggganaaacctcatgatagtctgtctcttcaaccaaaat	335
Db	367	catcgagagccatctgcacaagcggganaaacctcatgatagtctgtctcttcaaccaaaat	426
QY	336	tgtttgagagaaccctgaanaacccctgcacagagaagaatgtgtgtggaacaaagctccctgcg	395
Db	427	tgtttgagagaaccctgaanaacccctgcacagagaagaatgtgtgtggaacaaagctccctgcg	488

QY	396	aagagagagccacgctcagagagaagatcccgacatcggagctcagagagatctcgggaaa	455
Db	487	AAGAGCAGCCACGCTGAGAGAAAGTTCCCGCATCTGGAATACAGAGATTTTCGGGAAA	546
QY	456	cctcaaacccggcttcggaagctgagacgacgcaggaatctagctgacatccctgagc	515
Db	547	CCTCAACACCGGCTTCGGAAGCTGGACGACGACGAGGATTGAGTCATATCTCTGGC	606
QY	516	aacagctgagcctgcagcgcagatggtctgcgaacaacccgggtctgggcagagatctgcacccctga	575

Accession	Sequence	Position
Db	607 AACAGCTGGCGCTGCACCGGATGGCGGACCAACCGG-----	643
QY	576 ggaatgatgatgtaatctgttggccaaaggggaccttgggcgtggaagtgcgaagcagaagcca	635
Db	644 -----GTGGGGAGGGGGGCGCTTGGGCGCTGGGAAGTGTGGAGCCACAGACCA	687
QY	636 ggaacatcttgaaatctgttggatgtgtcttcgaacatcccgagaatcttgccttcgtgatcgc	695

DB	Sequence	Position
688	GGACATCTTGAGATCTGGTGGGTGTGCTGCACGATCCGAGACTCTGCTTCCTGCATGCC	747
696	TGAAGAGGCTCTCCTGAGGCACTTGAAGGAGGCTGCAAGTGTGCGAGTAGCCGTGCATAC	755

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DAN05YC03"
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/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-clo/dct primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for"

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LOCUS AL557370 942 bp mRNA EST 16-FEB-2001
 DEFINITION AL557370 LFI_FL012_TC1 Homo sapiens cDNA clone CS0DH004Y13 5 prime
 / mRNA sequence.
 ACCESSION AL557370
 VERSION AL557370.1 GI:12900909
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 942)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 JOURNAL Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 COMMENT Location/Qualifiers
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 /tissue_type="T cells from T cell leukemia"
 /lab_host="DH10B"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-stranded cDNA was digested with Not I and cloned
 into the Not I and Eco RV sites of the pCMVSPORT 6 vector.
 Library was constructed by Life Technologies. Contact :
 Feng Liang Life Technologies, a division of Invitrogen,
 9800 Medical Center Drive Rockville, Maryland 20850, USA
 Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 216 a 258 c 284 g 183 t 1 others
 ORIGIN

Query Match 66.7%; Score 690.4; DB 106; Length 942;
 Best Local Similarity 98.4%; Pred. No. 7e-174; Indels 4; Gaps 3;
 Matches 728; Conservative 1; Mismatches 7;

QY 1 atgagagtgatcgcgtggtgacccgcaagaccagctgtctgcacagacgagcagt 60
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 DB 191 atgagagtgatcgcgtggtgacccgcaagaccagctgtctgcacagacgagcagt 250
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 QY 61 gtgtgtgcaacatlgaaagcctgtaaccctgtgctgagcttgaaatcatgtctatgcc 120
 |||||||
 DB 251 gtgtgtgcaacatlgaaagcctgtaaccctgtgctgagcttgaaatcatgtctatgcc 310
 |||||||
 QY 121 accaagagggaacagaattcttgatactgactctctaaagaattggagaagaagccgtgtt 180
 |||||||
 DB 311 accaagagggaacagaattcttgatactgactctctaaagaattggagaagaagccgtgtt 370
 |||||||
 QY 181 accaagagcttgaaacatgccctgtgagaagaatgagctgtgtgttcaactctctg 240
 |||||||
 DB 371 accaagagcttgaaacatgccctgtgagaagaatgagctgtgtgttcaactctctg 430
 |||||||
 QY 241 aaggagctgtccactgtgtctctctctgcttcaaccatcgagacatctcgaaagcgagaa 300
 |||||||
 DB 431 aaggagctgtccactgtgtctctctctgcttcaaccatcgagacatctcgaaagcgagaa 490
 |||||||
 QY 301 aaacctcatgagctgtgtcttcttcaaccataaattgtgtggagaagaccctagaacctg 360
 |||||||
 DB 491 aaacctcatgagctgtgtcttcttcaaccataaattgtgtggagaagaccctagaacctg 550
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 QY 361 ccagagaagaagtgtgtgtggaaccagctccctgtcgagaagacagccagcttcgagaagaag 420
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 DB 551 ccagagaagaagtgtgtgtggaaccagctccctgtcgagaagacagccagcttcgagaagaag 610
 |||||||
 QY 421 ttccgcacatctgagcttcagagatctcgaggaaacatcaacacccgagcttcgagaagctg 480
 |||||||

DB 611 TTCGCCATCTGAGATTGACAGATTCGGGGAAACTCAACACCCGGCTTCGGAAGCTG 670
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 |||||||
 DB 671 gacgagcagcagagatctgagctcatctcgtgaaacagctgagcagcagctg 730
 |||||||
 QY 540 ctggcaaacacgggtgttgagacatccctgcaacctgagagatcatgctgtgagcca 599
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 DB 731 ctggcaaacacgggtgttgagacatccctgcaacctgagagatcatgctgtgagcca 790
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 QY 600 gggggccttgaggcgtgtgaaatgagcgaagacagcagcagcagcagcagcagc 659
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 DB 791 gggggccttgaggcgtgtgaaatgagcgaagacagcagcagcagcagcagcagc 849
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 QY 660 gctgacagatcccgagacgtctctcgtgacatgctgaaaggccttcaggacact 719
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 DB 850 gctgacagatcccgagacgtctctcgtgacatgctgaaaggccttcaggacact 907
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 QY 720 ggaaggaagctgcaatgtac 739
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 DB 908 tggaaagagcctcagctgtcc 927
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RESULT 7
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 LOCUS AL579416 LFI_FL012_TC1 Homo sapiens cDNA clone CS0DH004Y13 3 prime
 DEFINITION AL579416 LFI_FL012_TC1 Homo sapiens cDNA clone CS0DH004Y13 3 prime
 / mRNA sequence.
 ACCESSION AL579416
 VERSION AL579416.1 GI:12944439
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 838)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 JOURNAL Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 COMMENT Location/Qualifiers
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 /organism="Homo sapiens"
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 /lab_host="DH10B"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-stranded cDNA was digested with Not I and cloned
 into the Not I and Eco RV sites of the pCMVSPORT 6 vector.
 Library was constructed by Life Technologies. Contact :
 Feng Liang Life Technologies, a division of Invitrogen,
 9800 Medical Center Drive Rockville, Maryland 20850, USA
 Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 160 a 243 c 225 g 189 t 21 others
 ORIGIN

Query Match 65.9%; Score 682; DB 106; Length 838;
 Best Local Similarity 95.4%; Pred. No. 1.2e-171;
 Matches 702; Conservative 18; Mismatches 14; Indels 2; Gaps 2;

QY 300 aaacctcatgagctgtgtcttcttcaaccataaattgtgtggagaagaccctagaacct 359
 |||||||
 DB 838 aaacctcatgagctgtgtcttcttcaaccataaattgtgtggagaagaccctagaacct 780
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 QY 360 gccagagaagaagtgtgtgtggaaccagctccctgtcgagaagacagccagcttcgagaaga 419
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Db 779 GCCAGAAAGAGTGTGGGAAACACACTCCCTCCGGAAGAGACCCAGCTGCAGAGAAA 720
QY 420 gtcccgacatctgagatctcagagatctcgagaaacccaaacccggcttggaagct 479
Db 719 GTTCCCGCATCTGGAGTTCAGAGATATTCGGGAAACCTTAAACACCCGGCTTGGAAGCT 660
QY 480 ggaagcagcagcagagatctcagatcctcagcctcagcagcagcctgagcagcagc 539
Db 659 GGAGGAGCAGCAGAGAGTTCAGTCCATCATCTGGCAAGAGCTGGCTGAGGCAATGG 600
QY 540 ctgacacaaacgggttcggagacatctcagcctcagcagcagcctgagcagcagc 599
Db 599 CTGGCAACAAACGGGTGGGAGATCTGACACCTGAGGAATGATATGCTTGAGGCA 540
QY 600 gggagccttcggagctggaagctcgaagcgaagcagcagcctgagcagcagc 659
Db 539 GGGGCGCTTGCGGCTGGAAGTGGAGCAAGCAAGCAATCTTGATCTGGTGGTGT 480
QY 660 gctgcacgttcccgagacatctcagcctcagcagcagcctcagcagcagc 719
Db 479 GCTGCAGATCCCGAGACTCT-CTTCGTCATCTGTAAGGCGCTTCTGAGGCACT 421
QY 720 ggaagagagcagcagctgagcagcagcagcagcagcagcagcagcagcagc 779
Db 420 GGAAGAGAGCTGAGTGCAGTACCCCTGATACAGCTATGAGATGGCAACTGTA 361
QY 780 cctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 839
Db 360 CCTCATGAGAGASTCTGAGTCTAGACGCGCCAGATMCAACAAAGMCAATGCAAGC 301
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Db 300 TACATTCATGTCCTCTSCCAGCATGAAAGATGCGCTGAGATGAGCAACATTTGTASG 241
QY 900 catcactctgctgaacatccagcagcagcagcagcagcagcagcagcagcagc 959
Db 240 CATCAGCTGCTGATTCACAGAGGCGCCAGTTGGCTGCCAATCTTGATCTG 181
QY 960 cctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1019
Db 180 CCGGCAAAATGCTGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 121
QY 1020 gaacagatcccatca 1035
Db 120 TAACGATGCCSATTRA 105

RESULT 8
LOCUS BE547860 804 bp mRNA EST 09-AUG-2000
DEFINITION 601074758F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460575 5',
ACCESSION BE547860
VERSION BE547860.1 GI:9776505
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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Site: 2; Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
BASE COUNT 171 a 226 c 235 g 172 t
ORIGIN

Query Match 64.9% Score 671.4; DB 137; Length 804;
Best Local Similarity 94.0%; Pred. No. 8.1e-169;
Matches 742; Conservative 0; Mismatches 41; Indels 6; Gaps 4;

QY 8 tgattcggttggtaccgcaagagcagctgtcgcatacagaagcagctgtgtg 67
Db 1 TGATTGCGGTGGGTACCGCAAGAGCCAGCTTGCTGCATACAGCAGCATGTGTG 60
QY 68 caacatlaaaagcctcgtacccctgagcagcttggaatcattgtctcaccacag 127
Db 61 CAACATTAAGAGCCCTGACCTTGCCCTGCAAGTGAATCATGTGTCACACACAG 120
QY 128 ggaacaaagcttctgatactcagcagcagcagcagcagcagcagcagcagc 187
Db 121 GGAACAAGATCTTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 180
QY 188 agcttgaacacagcctcgtgagaagaatgaagtgaagtgtgttctcactccttgaaggcc 247
Db 181 AGCTTGAACAGCCCTGAGAAAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
QY 248 tgcacacgtctcctcctcctcctcctcctcctcctcctcctcctcctcctc 307
Db 241 TGCCACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 308 atgattcgtgtctctcctcctcctcctcctcctcctcctcctcctcctcctc 367
Db 301 ATGATGCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
QY 368 agagtggtggtggaacacagcctcctcgtgaagagcagcagcagcagcagcagc 427
Db 361 AGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 428 atctgagctcagagatcctcgtggaagcctcagcagcagcagcagcagcagc 487
Db 421 ATCTGAGTTCAGAGATGATTCGGGGAATCTCAACACCCGCTTGGAACTGACGAGC 480
QY 488 agcagaggttcagtgccatcctcgtggaacagcagcagcagcagcagcagcagc 547
Db 481 AGCAGAGTTCAGAGTTCATCTGCAACAGCTGCGCAGCGCATGGCTGCGACACA 540
QY 548 accggttcggaagatcctcagcagcagcagcagcagcagcagcagcagcagc 607
Db 541 ACCGGTGGGCGAGATCTCTGACCTGAGGAATGATGATGATGATGATGATGATGAT 600
QY 608 tgggctgtgagatgagcagcagcagcagcagcagcagcagcagcagcagcagc 667
Db 601 TCGGCTGTGAAGTGCAGAGCCAGCGCCAGACATCTTGATCTGATGATGATGATGAT 660
QY 668 atccgagagctgtg--cttcgcagcagcagc--aagggcctcctcgtgagcagc 723
Db 661 ATCCCAAGACTTGCTGCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGC 720
QY 724 -ggaagctcagctgt-gccagtagcgtgcatcagcagcagcagcagcagcagcagc 781
Db 721 CCGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780

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	11	111		
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LOCUS				
DEFINITION	AL520284	919 bp	mRNA	EST
AL520284	LTI_NFL004_NBC2		Homo sapiens	CDNA clone
CS0DB006Y607				
VERSION	AL520284			
KEYWORDS	AL520284.1	GI:12783777		
SOURCE				
ORGANISM	human			
REFERENCE	1			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	L1.N.B., Gruber.C., Jesse.J., and Polayes.D.			
JOURNAL	Full-length cDNA libraries and normalization			
COMMENT	Unpublished (2001)			
FEATURES	Contact: Genoscope			
Source	Genoscope - Centre National de Sequencage			
	BP 191 91006 Evry cedex - France			
	Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.			
	Location/Qualifiers			
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	/lab_host="DH10B"			
	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA			
	was primed with a NotI-Oligo(dt) primer. Five prime end			
	enriched, double-stranded cDNA was digested with Not I and			
	cloned into the Not I and Eco RV sites of the pCMVSPORT 6			
	vector. Library was normalized. Library was constructed			
	by Life Technologies. Contact : Feng Liang Life			
	Technologies, a division of Invitrogen 9800 Medical Center			
	Drye Rockville, Maryland 20850, USA Fax : (1) 301 610			
	8371 Email : fliang@lifetech.com URL :			
	http://fulllength.invitrogen.com"			
BASE COUNT	191 a	276 c	248 g	202 t
ORIGIN				2 others
Query Match	63.7%	Score 659.2	DB 105	Length 919;
Best Local Similarity	98.7%	Pred. No. 1.5e-165;		
Matches 705; Conservative	1;	Mismatches 4;	Indels 4;	Gaps 4;
QY	322	tttccacccaaaattgtgttggagaagccctagaaaccttgcagagaagaagtgtgttgga	381	
Db	918	YTTCAACCCAAATTTGTT- GGAAGACCCCTAGAAACCCCTCCAGAGAGTGTTG- GGA	861	
QY	382	accagctcccttgcgaagcgaagccagctgcagagaagtgtccgcatttgaattcaag	441	
Db	860	ACCACCTCCCTCGAAGACACGCCACGCTGCAGAGAAATTCCTCCGATCTGAGTTCAAG	801	
QY	442	agttctggggaacctcaacaccccgctctcggaaagtgcagagcagcaggaagttcaat	501	
Db	800	AGTATTTC- GGAAGAACTCAACACCCGGCTTCGGAAGCTGAGACGAGCAGGAGTTCACT	742	
QY	502	gccatcactcttgcgaacagctgtgcttgcagcgcattggtgcacaaacccgattggcag	561	
Db	741	GCATCATCTCTGGCAACACCTGGCTTCGACGCCATAGGGCTGCACAAACGGGTGGGCGAG	682	
QY	562	atctcgcaaccttgaagaatgcatatagctgtcgggtccaggggaccttggcgttgaagt	621	
Db	681	ATCTGCAACCTTGAGGAATGCAATGATGCTGTGGGCCAGGGGCCCTTGGGCGTTGGAAGTG	622	

Query Match	Score	DB	Length	801
62.88	650.4	DB 143	Length 801	

Best Local Similarity 99.7%; Pred. No. 3.3e-163;
Matches 662; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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OY 180 taccagaagagcttgacacatgctccgtagaagaatgaa-gtggacctgtgttctactcct 238
Db 1 TACCAAGAGAGCTTGAACATGCTCCCTGAGAAACATGAAATGAGACCTGTGTGTCTACTCTT 60
OY 239 tgaagagcctgcccacatgctctcctcctcctcctcctcctcctcctcctcctcctcct 298
Db 61 TGAAGAGAGCTGCTCCACATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
OY 299 aaaaacctcctatgctcgtctcctcctcctcctcctcctcctcctcctcctcctcctcct 358
Db 121 AAAACCTCATGATGCTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
OY 359 tgcgaagaagaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 418
Db 181 TGCAGAGAAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
OY 419 agtcccgacatctgagagctcagagatctcagagatctcagagatctcagagatctcagagat 478
Db 241 AGTTCCCGCATCTGTGAGATCTAGAGATCTAGAGATCTAGAGATCTAGAGATCTAGAGATCT 300
OY 479 tgaacagacagcagagatctcagatctcagatctcagatctcagatctcagatctcagatct 538
Db 301 TGACAGAGAGAGAGAGATCTAGATCTAGATCTAGATCTAGATCTAGATCTAGATCTAGATCT 360
OY 539 gctgagacaaacagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 598
Db 361 GCTGAGCAACAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
OY 599 agagagagcctctgagagctcagagatctcagagatctcagagatctcagagatctcagagat 658
Db 421 AGGGGCTTGGGCGTGGAGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
OY 659 tgcctgacagatccagagatctcagatctcagatctcagatctcagatctcagatctcagatct 718
Db 481 TCGTGCAGATCTCCAGAGATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
OY 719 tgaagagagcctcagatctcagatctcagatctcagatctcagatctcagatctcagatct 778
Db 541 TGAAGAGAGAGAGAGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCTG 600
OY 779 acctgacagagagagctcagatctcagatctcagatctcagatctcagatctcagatctcagatct 838
Db 601 ACCTACTGTGAGAGAGTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
OY 839 ctac 842
Db 661 CTAC 664

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RESULT 11
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LOCUS 601344923P1 NIH_MGC_Homo sapiens cDNA clone IMAGE:3677764 5',
DEFINITION mRNA sequence.
ACCESSION BE561357 GI:9805077
VERSION BE561357
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1136)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapdb-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov
Plate: LHC353 row: n column: 05
High quality sequence stop: 714.

FEATURES
source Location/Qualifiers
1..1136

/organism="Homo sapiens"
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EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 280 a 298 c 341 g 217 t
ORIGIN

Query Match 62.7%; Score 649.2; DB 137; Length 1136;
Best Local Similarity 94.8%; Pred. No. 7.6e-163;

Matches 713; Conservative 0; Mismatches 13; Indels 26; Gaps 3;

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Db 118 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 177
OY 121 accaagagagacagatctcagatctcagatctcagatctcagatctcagatctcagatctcagatct 180
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ACCESSION	BG469642		
VERSION	BG469642.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 835)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: csapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LILCM1460 row: g column: 23 High quality sequence stop: 824. Location/Qualifiers 1..835 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4661422" /clone_1id="NIH_MGC_15" /tissue_type="adenocarcinoma cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: colon; Vector: pORF7. Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."		
BASE COUNT	194 a 229 c 250 g 162 t		
ORIGIN			
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OY	121	accacagggacaagaattctgtatactgacactctccaagattgagagaagaacgttt	180
DB	283	ACCACAGGGGACAAGTTCTGTGATCTGCACCTCTCTAAGATTGGACAGAAGACCTG	342
OY	181	accaagaagcttgaacatgccctgtgaagaagaatgaagtgtgacctgtgttcaactcc	240

Db	343	ACCAAGGAGCTTTGAAACATGCGCCCTGAGAGAAATGAAAGTGAACCTGGTTGTTCACTTCCTTG	402
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Db	403	AAGGACGTCGCCACTGTGCTTCCTCTGCTTCAACACATCGGAGCCATCTGCAAGCGGAA	462
QY	301	aacctcatgatctgttcttcttcaacaaaattgtltggaagaccctagaacctg	360
Db	463	AACCTTCATGATGCTGTGTGTTCTTCCACCAAAATTTGTGGGAAGACCTTGAAACCTTG	522
QY	361	ccaagaagaatltgtgttggaaacacgccccttggaaagaagcccacatctcaagaagaag	420
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QY	481	gaacgaacgaagaagttcaagtgcacatcatcctgtgcaacagcgtgacctgacgcgaatggc	540
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Db	763	GGGGCTTGGGGCGTTGGGAAGTCCGAGCCCAAGGACCAAGACATCTTGATCT-GTGGGTCT	821
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VERSION	ALS20223.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	1 (bases 1 to 908)		
TITLE	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.		
JOURNAL	Full-length cDNA libraries and normalization		
COMMENT	Unpublished (2001)		
FEATURES	Genoscope - Centre National de Sequencage		
source	BP 191 91006 EVRI cedex - France		
	Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.		
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	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA		
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	cloned into the Not I and Eco RV sites of the pCMVSPORT 6		
	vector. Library was normalized. Library was constructed		
	by Life Technologies. Contact : Feng Liang Life		
	Technologies, a division of Invitrogen 9800 Medical Center		
	Drive Rockville, Maryland 20850, USA Fax : (1) 301 610		


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Oy 964 gccaaactgtctgctgcaagaagcacaacacatctgcatgtctgacgcaattgaac 1023
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Db 344 GCCACTTCTCTGCTGCAAGAGGACCAAAAATCTCTGATGTTGCACGGCAGCTTAAC 285
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LOCUS AUI32868 NT2RP4 Homo sapiens cDNA clone NT2RP400750 5', mRNA
DEFINITION sequence.
ACCESSION AUI32868.1 GI:10993407
VERSION AUI32868
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 812)
AUTHORS Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
        Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuko,Y. and
        Isogai,T.
        HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
        Saito,K., Yamamoto,T., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano
        S., Masuko,Y., Isogai,T.)
        Unpublished (2000)
JOURNAL Contact: Takao Isogai
COMMENT Genomics Laboratory
        Helix Research Institute
        1537-3 Yana, Kisarazu, Chiba 292-0812, Japan
        Tel: 81-438-52-3851
        Fax: 81-438-52-3952
        Email: genomics@hri.co.jp
        HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
        Research Institute; cDNA library construction; Department of
        Virology, Institute of Medical Science, University of Tokyo, and
        Helix Research Institute.
FEATURES
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BASE COUNT 193 a 226 c 241 g 152 t
ORIGIN

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Query Match 59.0%; Score 610.2; DB 108; Length 812;

Best Local Similarity 99.2%; Pred. No. 1,9e-152; Matches 634; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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Oy 121 accacagggacaagaattcttgaatactgacctctcaagattggagagaaagcctgttt 180
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Oy 481 gacgaagcagcagagttcagtgccatcatccttgcgaacagcctggcctgacgcagatgggc 540
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Db 655 GACGACAGCAGAGAGTTCAATGTCATCATCTCTGGCAACAGCTGGCTGCAGCCGATGGGC 714
Oy 541 tggcacaaccgggt-tgggcagatcctcgcaccctgaggaatgcatgtatgtctgtgggcca 599
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Search completed: October 6, 2001, 19:04:54
Job time: 522 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 17:37:53 ; Search time 90.47 Seconds
(without alignments)
2165.768 Million cell updates/sec

Title: US-09-601-138-1

Perfect score: 1035
Sequence: 1 atgagagtgctgcgcgtggg.....aattgacgagtcacattaa 1035

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	41.6	4.0	729	1	US-08-599-480-3 Sequence 3, Appl1
2	36.2	3.5	290	1	US-08-030-731A-41 Sequence 41, Appl1
3	36.2	3.5	290	1	US-08-030-731A-42 Sequence 42, Appl1
4	36.2	3.5	304	1	US-07-696-551B-12 Sequence 12, Appl1
5	35.6	3.4	7218	1	US-08-232-463-14 Sequence 14, Appl1
6	34.8	3.4	1889	2	US-08-946-241B-1 Sequence 1, Appl1
7	34.8	3.4	1889	2	US-08-946-241B-8 Sequence 8, Appl1
8	34.8	3.4	1889	2	US-09-309-053-1 Sequence 1, Appl1
9	34.8	3.4	1889	2	US-09-309-053-8 Sequence 8, Appl1
10	34.4	3.3	2502	1	US-08-073-384C-7 Sequence 7, Appl1
11	34.4	3.3	2502	1	US-08-254-359A-7 Sequence 7, Appl1
12	34.4	3.3	2502	1	US-08-483-043-7 Sequence 7, Appl1
13	34.4	3.3	2502	1	US-08-481-238-7 Sequence 7, Appl1
14	34.4	3.3	2502	2	US-08-471-066B-7 Sequence 7, Appl1
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25	34.2	3.3	729	4	US-09-140-804-10 Sequence 10, Appl1
26	34.2	3.3	2793	1	US-08-209-747-1 Sequence 1, Appl1
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30	33.6	3.2	2294	1	US-08-797-358B-1 Sequence 1, Appl1
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32	33.6	3.2	2790	2	US-08-448-250-4 Sequence 4, Appl1
33	33.4	3.2	359	3	US-08-589-028-3 Sequence 3, Appl1
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37	33.4	3.2	11219	3	US-08-439-009A-1 Sequence 1, Appl1
38	33.4	3.2	44377	2	US-08-804-227C-7 Sequence 7, Appl1
39	33.4	3.2	44377	2	US-08-804-198-1 Sequence 1, Appl1
40	33.2	3.2	1201	6	5252556-2 Patent No. 5252556
41	33	3.2	281	1	US-07-764-655D-12 Sequence 12, Appl1
42	33	3.2	281	1	US-07-764-655D-13 Sequence 13, Appl1
43	33	3.2	281	6	5514646-1 Patent No. 5514646
44	33	3.2	3579	1	US-08-674-168-15 Sequence 15, Appl1
45	33	3.2	3579	3	US-08-985-908-18 Sequence 18, Appl1

ALIGNMENTS

RESULT 1

US-08-599-480-3/C

Sequence 3, Application US/08599480

Patent No. 5753459

GENERAL INFORMATION:

APPLICANT: Bianco, David R.

APPLICANT: Miller, James N.

APPLICANT: Lovett, Michael A.

APPLICANT: Champion, Cheryl I.

APPLICANT: Tempst, Paul J.

TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF A

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: California

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/599,480

FILING DATE: 23-JAN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Leairn, June M.

REGISTRATION NUMBER: 31,238

REFERENCE/DOCKET NUMBER: 07419/018001 (CIP of 016001)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 678-5070

TELEFAX: (619) 678-5099

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 729 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:

CLONE: TROMP2

FEATURE:

NAME/KEY: CDS

LOCATION: 1..726

US-08-599-480-3

Query Match 4.0%; Score 41.6; DB 1; Length 729;
Best Local Similarity 47.3%; Pred. No. 0.0058;
Matches 125; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

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QY 236 gggaaacacctcagatgctgtg 319
DB 188 GCGAAGCCCTTGTGATGAACTTG 165

RESULT 2
US-08-030-731A-41
Sequence 41, Application US/08030731A
Patent No. 5426036
GENERAL INFORMATION:
APPLICANT: Koller, Klaus-Peter
APPLICANT: Riebs, Guenther Johannes
APPLICANT: Uhlmann, Eugen
APPLICANT: Walmeier, Holger
TITLE OF INVENTION: Processes for the Preparation of Foreign
NUMBER OF INVENTIONS: Proteins in Streptomyces
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinagan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030.731A
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/189,840
FILING DATE: 03-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/430,622
FILING DATE: 01-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/687,610
FILING DATE: 19-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,757
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 37 14 866.4
FILING DATE: 05-MAY-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 38 37 273.8
FILING DATE: 03-NOV-1988

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 39 27 449.7
FILING DATE: 19-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 12 818.0
FILING DATE: 21-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kirscher Michael K.
REGISTRATION NUMBER: 34,851
REFERENCE/DOCKET NUMBER: 02481-0593-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-030-731A-41

Query Match 3.5%; Score 36.2; DB 1; Length 290;
Best Local Similarity 46.6%; Pred. No. 0.15;
Matches 116; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 485 agcagcagagatcagtcacatcctcctgcaacaagctgctcagcagcagctgagc 544
DB 20 ACCGACCTCTGGGGCTCCACCTAGTGAAGCTCTTACTCTGCTGCGGGAGGAG 79
QY 545 acaacccgggttgagcagatcctgcacacctgaggaatgagtatgctgtgagcagagg 604
DB 80 GCTTCTTACACACCCAGAGCCCGGGAGGAGAGAGACCTTCAGTGGGAGGTGG 139
QY 605 ccttgagcgtggaagtgcagagcaagagcaagacatcttgatctgtgtgtgtgtgc 664
DB 140 AGCTGGGGGGGGCCCTGGGCGCAGGACCTGCGACCCCTTGGCCCTGAGGGGCTCCTGC 199
QY 665 acgatccagagactgcttcgtcgtcagctgtaagaggccttcctgaagcacttgaa 724
DB 200 AGAAGCGCGGATGCTGAGCAGTGTGACACGACATCTGCTCTTACACAGCTGAGA 259
QY 725 gagcgtgca 733
DB 260 ACTACTGCA 268

RESULT 3
US-08-030-731A-42/c
Sequence 42, Application US/08030731A
Patent No. 5426036
GENERAL INFORMATION:
APPLICANT: Koller, Klaus-Peter
APPLICANT: Riebs, Guenther Johannes
APPLICANT: Uhlmann, Eugen
APPLICANT: Walmeier, Holger
TITLE OF INVENTION: Processes for the Preparation of Foreign
NUMBER OF INVENTIONS: Proteins in Streptomyces
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinagan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/030,731A
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/189,840
FILING DATE: 03-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/430,622
FILING DATE: 01-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/687,610
FILING DATE: 19-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,757
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 37 14 866.4
FILING DATE: 05-MAY-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 38 37 273.8
FILING DATE: 03-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 39 27 449.7
FILING DATE: 19-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 12 818.0
FILING DATE: 21-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kitschner Michael K.
REGISTRATION NUMBER: 34,851
REFERENCE/DOCKET NUMBER: 02481-0593-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5..290
OTHER INFORMATION: /note="Sequence ID No. 5426036 42 is
OTHER INFORMATION: complementary to Sequence ID No. 5426036 41 at positions
OTHER INFORMATION: 5-290 of Sequence ID No. 5426036 41."
IS-08-030-731A-42

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[illegible]

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Db          35 ACTACTGCA 27          |||||
                                           RESULT 4
US-07-696-551B-12          : Sequence 12, Application US/07696551B
Patent No. 5232841
GENERAL INFORMATION:
APPLICANT: Hashimoto, Tamotsu
APPLICANT: Tsujimura, Atsushi
APPLICANT: Ueda, Shigeo
TITLE OF INVENTION: Process for Preparing Peptide
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/PC-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/696,551B
FILING DATE: 19910509
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-122166
FILING DATE: 11-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-334575
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence M. Lavlin, Jr.
REGISTRATION NUMBER: 30,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-696-551B-12

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Query Match	3.5%	Score 36.2	DB 1	Length 304
Best Local Similarity	46.6%	Pred. No. 0.15		
Matches 116	Conservative	0	Mismatches 135	Indels 0
			Gaps 0	
QY	485	agcagcaggagattcagtcagtcacatccctcgtgcagcagcatcgtgc	544	
Db	43	accagcacccttgccggcccccaccactaggaagctctcactggctggcggagcag	102	
QY	545	acacacccggttcgggcagatctctgcaccccttcaggaatgcattgctctgtggccagcgggg	604	
Db	103	gcctttcttcacacaccccaagaccgccccgggaagcagagaccctcagctggcggcagctgg	162	
QY	605	ccttgcgcgttgaaagctgcagcagcaagagacatcttgatcttcgttgcgttcgc	664	
Db	163	agctggcggcggcccttcggccagcagcagccttcacaccccttggcggcggaggggtcccttc	222	
QY	665	acgatcccgagagactcgtccttcgtcgcacatcgctcgaagaagccttccttcagcaccctcggaag	724	
Db	223	agaaacggcgccctctcgttcgacagctctgcacacagcactctgccttcacacgctggaca	282	

OY	725	gagcctgca	733
Db	283	ACTACTGCA	291

RESULT 5
US-08-232-

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1 Sequence 14, Application US/08232463
2 Patent No. 5670367
3
4 GENERAL INFORMATION:
5
6 APPLICANT: DORNER, F.
7 APPLICANT: SCHEFFELINGER, F.
8 APPLICANT: FALKNER, F. G.
9 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
10 NUMBER OF SEQUENCES: 52
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Foley & Lardner
13 STREET: 1800 Diagonal Road, Suite 500
14 CITY: Alexandria
15 STATE: VA
16 COUNTRY: USA
17 ZIP: 22313-0299
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: PatentIn Release #1.0, Version #1.25
24
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08/232,463
27 FILING DATE:
28
29 CLASSIFICATION: 435
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US/07/935,313
32 FILING DATE:
33
34 FILING DATE: 26-AUG-1991
35 APPLICATION NUMBER: EP 91 114 300.6
36 FILING DATE:
37
38 ATTORNEY/AGENT INFORMATION:
39 NAME: BENT, Stephen A.
40 REGISTRATION NUMBER: 29,768
41 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
42 TELECOMMUNICATION INFORMATION:
43 TELEPHONE: (703)836-9300
44 TELEFAX: (703)683-4109
45
46 TELEX: 899149
47
48 INFORMATION FOR SEQ ID NO: 14:
49 SEQUENCE CHARACTERISTICS:
50 LENGTH: 7218 base pairs
51 TYPE: nucleic acid
52 STRANDEDNESS: single
53 TOPOLOGY: linear
54
55 IMMEDIATE SOURCE:
56
57 CLONE: PTZ9PL-F15
58
59 US-08-232-463-14

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Query Match      3.48; Score 35.6; DB 1; length 7218;
Best Local Similarity 3.38; Pred. No. 1.1;
Matches 11; Conservative 184; Mismatches 143; Indels 0; Gaps 0

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QY 340 gggaaagaccccttaaaaaccgcgcaagaagatgtgtgttggaaccgatcctctcgaaaga 399
::: ::::::::::
Db 1386 rr 1327
:::::
OY 400 gccagccagctgcagagaaagtcccgcattgtagtctaggagatactgggaaacc 459
::: ::::::::::
Db 1326 rr 1267
:::::
OY 460 aaacaccgacttcggaagctygaaagcgacagagatlcaagtcacalcatcctycaaca 519
::: ::::::::::
Db 1266 rr 1207
:::::
OY 520 gcgcgacctgagagcacttggtctbgcacaaaccggttgtgcagatcctgcacctyagaa 579

[illegible]

RESULT 6
US-08-946-

```

1 Sequence 1, Application US/08946241B
2 Patent No. 5928941
3
4 GENERAL INFORMATION:
5 APPLICANT: Lee, Mu-En
6 APPLICANT: MGA Nulty, Megan M.
7 TITLE OF INVENTION: REPRESSOR KRPPPEL-LIKE FACTOR
8 NUMBER OF SEQUENCES: 13
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Fish & Richardson P.C.
11 STREET: 225 Franklin Street
12 CITY: Boston
13 STATE: MA
14
15 COUNTRY: USA
16 ZIP: 02110-2804
17
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: Diskette
20 COMPUTER: IBM compatible
21 OPERATING SYSTEM: DOS
22 SOFTWARE: FASTSEQ Version 2.0
23
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/946,241B
26 FILING DATE: 07-OCT-1997
27
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 60/030,035
30 FILING DATE: 05-NOV-1996
31 APPLICATION NUMBER: 60/027,521
32 FILING DATE: 07-OCT-1996
33 ATTORNEY/AGENT INFORMATION:
34 NAME: Creason, Gary L.
35 REGISTRATION NUMBER: 34,310
36 REFERENCE/DOCKET NUMBER: 05433/027001
37 TELECOMMUNICATION INFORMATION:
38 TELEPHONE: 617-542-5070
39 TELEFAX: 617-542-8906
40
41 INFORMATION FOR SEQ. ID NO.: 1:
42
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 1889 base pairs
45 TYPE: nucleic acid
46 STRANDEDNESS: single
47 TOPOLOGY: linear
48
49 FEATURE:
50
51 NAME/KEY: Coding Sequence
52 LOCATION: 434...1843
53
54 US-08-946-241B-1

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Query Match	3.48;	Score 34.8;	DB 2;	Length 1889;
Best Local Similarity	52.88;	Pred. No. 0.99;		
Matches 75;	Conservative 0;	Mismatches 67;	Indels 0;	Gaps 0

QY	608	tgagcgtggagagatgcgagccaaagagaccagacactcttgatctgctgagtgctgcagac	667
Db	1434	TGGGATGGAAGCCGGGAGAACCCGGCAGGCGTACATCCCTGCTGTACACT	1375
QY	668	atcccgagactcgcctcgcctcatcgcctgaaaagggccttcctgaagcactctgaagaag	727
Db	1374	TCTCTAAGACCCACAGGGTCTGGGATAGTCTGTCGGAGCTGGCCGCCACGGGGAGATCG	1315

CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,359A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 06-JUN-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-254-359A-7

Query Match 3.3%; Score 34.4; DB 1; Length 2502;
Best local Similarity 44.0%; Pred. No. 1.5;
Matches 128; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 413 agagaaagttccgcacatctggaagttcagagatctcgaggaaacctcaacccgcttc 472
1232 AGAGGCTCTCCGACGCTNNNGCAGCGCTTGAGGGGAGAGAGGCTCTTGCTT 1291
QY 473 ggaagcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 532
1292 ACCAGGAGGTGAGAGAGCCCTTCCGGGCTCTGAGCCCATGAGGCCACGGGGTTC 1351
QY 533 gcatggcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 592
1352 GCGTGACGTGGCTACCTTCAGAGCCCTTTCCTGAGAGTGGGGAGAGATCCGCCGC 1411
QY 593 tgggcaaggaggccttgaggcgttgaaagtgagagcagcagcagcagcagcagcagc 652
1412 TCAGAGAGAGGCTCTCCGCTGCGGCCACCCCTTCAACCTCAACTCCCGGACACG 1471
QY 653 tgggtgtgtcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 703
1472 TGGAAAGGCTCTTTCAGAGAGCTGAGGCTTCCGCCCATCGGCAAGACGG 1522

RESULT 12
US-08-483-043-7
Sequence 7, Application US/08483043
Patent No. 5691142
GENERAL INFORMATION:
APPLICANT: Dahlberg, James E.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:

ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,043
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-00613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-483-043-7

Query Match 3.3%; Score 34.4; DB 1; Length 2502;
Best local Similarity 44.0%; Pred. No. 1.5;
Matches 128; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 413 agagaaagttccgcacatctggaagttcagagatctcgaggaaacctcaacccgcttc 472
1232 AGAGGCTCTCCGACGCTNNNGCAGCGCTTGAGGGGAGAGAGGCTCTTGCTT 1291
QY 473 ggaagcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 532
1292 ACCAGGAGGTGAGAGAGCCCTTCCGGGCTCTGAGCCCATGAGGCCACGGGGTTC 1351
QY 533 gcatggcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 592
1352 GCGTGACGTGGCTACCTTCAGAGCCCTTTCCTGAGAGTGGGGAGAGATCCGCCGC 1411
QY 593 tgggcaaggaggccttgaggcgttgaaagtgagagcagcagcagcagcagcagcagc 652
1412 TCAGAGAGAGGCTCTCCGCTGCGGCCACCCCTTCAACCTCAACTCCCGGACACG 1471
QY 653 tgggtgtgtcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 703
1472 TGGAAAGGCTCTTTCAGAGAGCTGAGGCTTCCGCCCATCGGCAAGACGG 1522

RESULT 13
US-08-481-238-7
Sequence 7, Application US/08481238
Patent No. 5795763
GENERAL INFORMATION:
APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:

Search completed: October 6, 2001, 17:39:53
UD time: 120 sec

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: NUMBER OF SEQUENCES: 114
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
: STREET: 220 MONTGOMERY STREET, SUITE 2200
: CITY: SAN FRANCISCO
: STATE: CALIFORNIA
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 94104
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,956
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/402,601
: FILING DATE: 09-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/337,164
: FILING DATE: 09-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/254,359
: FILING DATE: 06-JUN-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/073,384
: FILING DATE: 04-JUN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/986,330
: FILING DATE: 07-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: CARROLL, PETER G.
: REGISTRATION NUMBER: 32,837
: REFERENCE/DOCKET NUMBER: FORS-01801
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 705-8410
: TELEFAX: (415) 397-8338
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2502 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
:
: US-08-484-956-7

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Query Match          3.3%; Score 34.4; DB 2; Length 2502;
Best Local Similarity 44.0%; Pred. No. 1.5; Mismatches 163; Indels 0; Gaps 0;
Matches 128; Conservative 0;

QY 413 agagaagttccgcagctcgtgagttcagagatctcggggaaccctcaacaccggtc 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1232 AGAGGCTCTTCGAGACTNNNGACAGCGCTTGAGGGGAGAGAGGCTCTTGCTTT 1291
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 473 ggaagctggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1292 ACCAGAGGCTGGAGAGCCCTTTCCCGGCTCCTGGCCACATGAGGCCACGCGGCTNC 1351
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 533 gcatggctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 592
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1352 GCGTGGACCTGGCTACCTCCAGCCCTTTCCTGAGGCTGGGAGAGATCCGCCGCC 1411
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 593 tgggccaaggaggccttggtgctggaagtgcagccaaggccaaggccaagcatcttgatctg 652
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1412 TCGAGAGAGAGGCTCTCCGCTGGCCGCCACCCCTTCAACCTCAACTCCCGGAGCCAGC 1471
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 653 tgggtgtgtcgaagatcccgagactgtcttcgtgtcatgtcgtgaagg 703
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1472 TGGAAAGGCTCTTTGAGAGACTNGGCTTCCGCCCATCGGCAAGACGG 1522
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This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 19:04:54 ; Search time 1970.35 Seconds
(without alignments)
3339.674 Million cell updates/sec

Title: US-09-601-138-12

Perfect score: 1113

Sequence: 1 cacacagccacttccaag.....aattgaacagatgcccatata 1113

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1022815 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
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7: gb_est7:*
8: gb_est8:*
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11: gb_est11:*
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74: em_esthum40:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

QY	661	atctatgctcttgaggccaggaggagcttgaggcttgaaatgctgagccaaagaccagagacac	720
Db	761	atgtatgctcttgaggccaggaggagcttgaggcttgaaatgctgagccaaagaccagagacac	820
QY	721	tggatctggtgggtgctgctgacgacatcccgagagctgctgctgctgcatgctgaaag	780
Db	821	ttggatctggtgggtgctgctgacgacatcccgagagctgctgctgctgcatgctgaaag	880
QY	781	gacctctgaggacaccttgaaagagagctgagtgctgacagtaagccgtgcatagacatg	840
Db	881	gacctctgaggacaccttgaaagagagctgagtgctgacagtaagccgtgcatagacatg	939
QY	841	aagagtgaggagacacctgac	900
Db	940	aagagtgaggagacacctgac	998
QY	901	caagagac	936
Db	999	caagagac	1032
RESULT	2		
AL524270			
LOCUS	AL524270	882 bp	mRNA
DEFINITION	AL524270 LTR_NFL003_NBC3	Homo sapiens	cdna clone CSDDC002Y01 5
ACCESSION	AL524270		
VERSION	AL524270.1	GI:12787763	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1. (bases 1 to 882)		
JOURNAL	Li W.B., Gruber,C., Jesse,J. and Polayes,D.		
COMMENT	Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope Genoscope - Centre National de Sequenage BP 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.		
FEATURES			
source			
	1..882		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="CSDDC002Y01"		
	/clone_1lb="LTR_NFL003_NBC3"		
	/sex="male"		
	/tissue_type="neuroblastoma cells"		
	/lab_host="DH10B"		
	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Peng Liang Life Technologies, a division of Invitrogen 9800 Medical Centre Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@life.com URL : http://fulllength.invitrogen.com"		
BASE COUNT	205 a	236 c	262 g
ORIGIN			178 t
			1 others

Query Match	75.28;	Score 837.4;	DB 105;	Length 882;
Best Local Similarity	99.28;	Pred. No. 4.5e-214;		
Matches 852; Conservative	0;	Mismatches 6;	Indels 1;	Gaps 1

y 253 ctgcttaccgaagagcctgaaacatgccctggagaagaaatgaagtgaacctgtttgttcac 312
 Db 1 CTGTTTACCAAGAGCCTGAACATGCCCTGGAGAAGAAATGAAGTGACCTGTGTTTCAC 60

QY	313	tccttgaagaactgtcccaactgtgtctccctccctgtgtcaacatctgaag	372
Db	61	tccttgaagaactgtcccaactgtgtctccctccctgtgtcaacatctgaag	120
QY	373	cgggaanaaccctcaatgactgttgtcttcttccaccbaaatttgttgaagaccctaga	432
Db	121	cgggaanaaccctcatgatgtctgtgttcttccaccbaaatttgttgaagaccctaga	180
QY	433	acccttcacgaagaagtgctgtgtgtgaacacagctccctctgaaagcaaccagctgcag	492
Db	181	acccttcacgaagaagtgctgtgtgtgaacacagctccctctgaaagcaaccagctgcag	240
QY	493	agaaagtccccgcatcttgagtgatctcagagtatctcggsgaaaccttcaaccggcgttcag	552
Db	241	agaaagtccccgcatcttgagtgatctcagagtatctcggsgaaaccttcaaccggcgttcag	300
QY	553	aagcttgacgaagcagcagagtgctcagtgccatcatccctctgcaacagctgacctgcacgc	612
Db	301	aagcttgacgaagcagcagagtgctcagtgccatcatccctctgcaacagctgacctgcacgc	360
QY	613	atggagctgacaaacccggcttgaggacatccctgcgaacccctggaagaaatgcaatgtctgtg	672
Db	361	atggagctgacaaacccggcttgaggacatccctgcgaacccctggaagaaatgcaatgtctgtg	420
QY	673	ggccgaaggggccttgggcgttggaagtcgagacgaagagacacagacaactgtgactgtgtg	732
Db	421	ggccgaaggggccttgggcgttggaagtcgagacgaagagacacagacaactgtgtgtgtg	480
QY	733	ggtgtgtgtcgaagatcccgagaactctgtcttgcgtgcatacgtctgaaggccttcctgaag	792
Db	481	ggtgtgtgtcgaagatcccgagaactctgtcttgcgtgcatacgtctgaaggccttcctgaag	540
QY	793	caacctgaaaggagctgtcagtgctgcagatagacgtgcatacagctcctgaaggatctggaa	852
Db	541	caacctgaaaggagctgtcagtgctgcagatagacgtgcatacagctcctgaaggatctggaa	599
QY	853	ctgtacctgactctgaaggagctctggaagctcagaacgtctcagatagacatacaagaagccatg	912
Db	600	ctgtacctgactctgaaggagctctggaagctcagaacgtctcagatagacatacaagaagccatg	659
QY	913	caggcttaccatccatgtctcccttgcggcaagaatgaagatgtgcccctggaagatgaaaccaacgtg	972
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QY	973	gtgaagcatcaactgtcgttacaatcttcacgaaggagccccaatgtgctgcgccagaaactctggc	1032
Db	720	gtgaagcatcaactgtcgttacaatcttcacgaaggagccccaatgtgctgcgccagaaactctggc	779
QY	1033	atcagacctggcacaactgtgtctgcgaacaaaggagccaaanaacatccctgtgtgcacgg	1092
Db	780	atcagacctggcacaactgtgtctgcgaacaaaggagccaaanaacatccctgtgtgtgcacgg	839
QY	1093	caattgaacgaatgccatt	1111
Db	840	cagccttaacgatgccatt	858

RESULT	3
AL557370	
LOCUS	AL557370 942 bp mRNA EST 16-FEB-2001
DEFINITION	AL557370 LTI.FL012_TCl Homo sapiens CDNA clone CS0DH004YP13 5 prime , mRNA sequence.
ACCESSION	AL557370
VERSION	AL557370.1 GI:12900909
KEYWORDS	EST,
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 942)
AUTHORS	Ll.M.B., Gruber,C., Jesssee,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: sequef@genoscope.cns.fr. Web : www.genoscope.cns.fr.

FEATURES

source

1..942
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODH004P13"
/clone_lib="LRI_F1012.TC1"
/tissue_type="T cells from T cell leukemia"
/lab_host="DH10B"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 216 a 258 c 284 g 183 t 1 others
ORIGIN

Query Match 68.0% Score 756.4; DB 106; Length 942;

Best Local Similarity 98.4% Pred. No. 2.6e-192;

Matches 805; Conservative 1; Mismatches 7; Indels 5; Gaps 4;

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Oy 1 cacacagcacttcccaagcagagcactgtctgttaacgcacatgcgctcgaacgagc 60
Db 114 CACACAGCCTACTTCCCAAGCGGA-CCATGCTCGTACGCGCAATCGGCTGCAACGGG 172
Oy 61 gaagaaagagcccaagatgagatgattcgctgtgttaaccgcaagagcagcttgc 120
Db 173 GAAGAAAGAGCCCAAGATGAGATGATTCGGTGGTGAACCGCAAGCCGCTTGGCT 232
Oy 121 ccatacagacgacagctgtgtgcaacatgaaagcctgtacccctgcgcagctt 180
Db 233 CCGATACACACGACAGCTGTGTGSCACATTCGAAGCCTCGACCTGGCCGCAATT 292
Oy 181 gaatcatgtctatgtccacacaggggacaagatctctgatactgactcttaagat 240
Db 293 GAATCATGTGATGTCCACACAGGGGACAAGATTCCTGATCTGCACCTCTAAGATT 352
Oy 241 ggaagaaagagcctgttcccaagagccttgaacatgcccctggagagaagaatgagc 300
Db 353 GGAGAAAGAGCCTGTTTACCAAGAGCTTGAACATGCCCTGGAGAAGATGAAGTGAC 412
Oy 301 ctggttctcaactccttgaagacctgcacactgtctccctcctgcttccacatcgga 360
Db 413 CTGTTGTTCACTCTTGAAGACCTGCCACTGTCTTCTCTGCTTCCACCATCGGA 472
Oy 361 gccatctgaagcgggaaaaaccctcagatgtctgtctcttccacaaaatttgttgg 420
Db 473 GCCATCTGCAAGGGGGAAAAACCTCATGATGCTGTCTTCCACCAAAATTTGTTGG 532
Oy 421 aagacccctagaacccctgcagagaagaagtgtgttggaacccgcctctggcgaagga 480
Db 533 AAGACCCCTAGAAACCTTGCAGAGAGAGTGTGTGGAAACCGCTCCCGCAAGAGCA 592
Oy 481 gccacatgcagagaagctcccgcactctgaagctcagagatattcggggaaaaccctaac 540
Db 593 GCCCAGCTGAGAGAAAGTTCCCGCATCTGAGATTCAAGAGATTTGGGAAACCTCAAC 652
Oy 541 acccgcttcgaagcttgaagcagcagagagttcagtgcacatcctctgcaacagct 600
Db 653 ACCCGCTTCGGAAGCTGAGAGCAGAGAGTTCAGTCCATCATCCGCGCAACAGCT 712
Oy 601 ggccttcagcagcagtg-ggcttgacaaacgggttggcagatccttcaacctgaagaa 659
Db 713 GGCCTGACAGGCACTGTGCTGGCAACCGGGGTGGGCAATCTCCACCTGAGGAATG 772

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Oy 660 catgatctgttgagccagagggccttggcggtgaaatgctgagccaaagaccagacat 719

Db 773 CATGATGCTGTGGCGCCAGGGGG-CTTGGCGGTGGAAGTGCAGCCAGACACAGACAT 831

Oy 720 ctggaatctgt 779

Db 832 CTGTGATCTGTGGGT 891

Oy 780 ggccttcctgagcagccttgaagagagctgcagctgac 817

Db 892 GCGTTCCTGAG--CACCTGGAAGAGCTGCAGTGTGC 927

RESULT

4

LOCUS BG337601 904 bp mRNA EST 27-FEB-2001
DEFINITION 602435148F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4553315 5',
mRNA sequence.

ACCESSION BG337601
VERSION BG337601.1 GI:13144039

KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC http://mgc.nhl.nih.gov/
1 (bases 1 to 904)

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-riemail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate: LCM1250 row: 0 column: 12
High quality sequence stop: 768.

FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="Organ: uterus; Vector: pOTB7; Site: 1; XhoI; Site: 2; EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT 212 a 234 c 285 g 171 t 2 others
ORIGIN

Query Match 65.4% Score 728.4; DB 152; Length 904;

Best Local Similarity 98.6% Pred. No. 8.4e-185;

Matches 765; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

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Oy 233 ctaagattgagagaagcgtgttaccagaagagcttgaacatgcccctggagaagaatg 292
Db 2 CTAAAGATTGAGAGAAAGCCTGTTACCAAGAGAGCTTGAACATGCCCTGAGAGAAATG 61
Oy 293 aatgagacctggtgttcaactcttgaagagactgcccactgtgcttccctcggttca 352
Db 62 AAGTGACCTGTTGTTCACTCTTGAAGAGACCTGCCCACTGTGCTTCCCTGCTTCA 121

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[illegible]

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/notes="Organ: colon; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT      194 a      229 c      250 g      162 t

ORIGIN

Query Match      65.1%; Score 724.4; DB 154; Length 835;
Best Local Similarity 99.6%; Pred. No. 9, 8e-184;
Matches 747; Conservative 0; Mismatches 1; Indels 2; Gaps 2

QY      1  ccaacgcctactttcccaaggagaccatgctcgtgtaacggaatgagcctgcgaacgagc 60
DB      85  CACACGCTACTCTTCCAAAGCGAGCGCACTGTGGTAAACGCAATGCGCTCCAAACGCGC 144

QY      61  gaagaaacagcccaagaatgtagatgctgcgtggtgacccgcaagagcagcttct 120
DB     145  GAAAGAAACAGCCCAAGATGAGAGTGATTCGGCTGGTATCCCGCAAGACCAAGCTTGT 204

QY     121  cgcatacagaacggaagctgtggtggtgcaacatgaaagcctgtaacctgacctgcagttt 180
DB     205  CCGCATACACACGCGACAGTGTGGTGCAACATGAAAGCCTCGTACCCCTGCGCTGAGTTT 264

QY     181  gaatcatctgcatctcccaaggaggaagatcttctgaacagcactcctaagatt 240
DB     265  GAAATCATTTGCTATGTGCGCACACAGGGGACCAAGATTTCTTGAATCTCTTAAGATT 324

QY     241  ggaagagaaagacgctgtctacaaaggagctctgacaatgcctctgagaagaatgaatgtagc 300
DB     325  GGAGAGAAAGAGCTGTTTACCAAGAGCGTTGAACATGCCCTGGAGAGATGAATGAGAC 384

QY     301  ctggtgttcatctcctcttgaaggaacctgcccactgtgctctcctcgtgctcaacatcgga 360
DB     385  CTGTGTGTTCACTCTTGAAGGACCTGCCCACTGTGCTTCCCTGCTTCACCATCGCA 444

QY     361  gccatctgcaagcgggaaaacctcatgtagtctgtctgtctcttcacacaaatcttctgg 420
DB     445  GCCATCTGCAGACGGGAAACCCCTCATGATGCTGTGTTGCTTTACCCCAAAATTTTGTGG 504

QY     421  aagaacctcctaaacccctgcagagaagaagtgtgtgtggaacagctccctcgcgaagaca 480
DB     505  AAGACCTTAAGAAACCTTCGCACAGAAAGATGTGTGGGAAACCAAGCTCCCTCGGAAGACA 564

QY     481  gccacgctgcagagaagaatctccgcgcatctgtaggtctcagaagatctcgggagaacctcagc 540
DB     565  GCCCAGCTGCAGAGAAAGTCTCCCGCATCTGAGATTCTCAGAGATATTCGGGAAACCTCAAC 624

QY     541  acccgagcttcggaagctggaacgagcagcagaagatctcagltgcatacatcctgycacaagct 600
DB     625  ACCCGGCTTCGGAACCTGCAGACAGCAGCAGGATGTTCAATGCGCATCATCTCTGCAACAGCT 684

QY     601  gaccgcagcgcatagtgctctgcaacaacggggtctggcgacatctcgcaccccgaggaatgac 660
DB     685  GGCCTGCAGACCGCATGTGGCTGGCAACACGGGTGGGCGAGATCTTCACCTTGAGAAATGC 744

QY     661  atgtatgtctgtgagcaggggaccttgggcg-ctgaaatctgcagcgaagacaggaacat 719
DB     745  ATGTATGCTGTGGGCGCAGGGGGCCTTTGGCGCTTGGAAATCGCAGACCAAGCAGACAT 804

QY     720  cttagatctggttggtgtgtgtgtgacagatcc 749
|||||

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Db	805	CTGTGATCT-GTGGGTGTGCTGAACGATCC	833
RESULT	6		
AL561865/c			
LOCUS	AL561865	949 bp	mRNA
DEFINITION	AL561865	LT1_NF004_NBC2	Homo sapiens CDNA clone CS0DB006Y103
ACCESSION	AL561865		
VERSION	AL561865.1	GI:12909719	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	L.W.B., Gruber,C., Jessee,J. and Polayes,D.		
TITLE	Full-length CDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqlife@genoscope.cns.fr , www.genoscope.cns.fr .		
FEATURES			
source	Location/Dualifiers 1..949 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CS0DB006Y103" /clone_lib="LT1_NF004_NBC2" /sex="male" /tissue_type="neuroblastoma cells" /lab_host="DH10B" /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: liang@lifetech.com URL: http://fulllength.invitrogen.com "		
BASE COUNT	196 a	277 c	265 g
ORIGIN		207 t	4 others
Query Match	63.9%	Score 711.4	DB 106; Length 949;
Best Local Similarity	98.6%	Pred. No. 3.1e-180;	
Matches	756; Conservative	3; Mismatches	4; Indels 4; Gaps 4;
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OY	407	caaaatctgttggaagagcccttagaagccctccagagaagagtggtgtggaaccagct	466
DB	882	CAAAATTTGTT-GGAAGACCTCTAGAAACCCCTCCAGAGAGAGTGTGGGACCAAGCT	824
OY	467	ccctcgagaagagcaaccagctctcagagaagaattccgcacatctggagtccagagatattc	526
DB	823	CCCTCGGAAGACGACGCCAGCTGCAGAGAGAAATTCGCCGATCTGGAGTTCCAGAGATTTC	764
OY	527	ggggaaacctcaaccgccggtctgggaagctggaagcagcagcagaagttcagttccatca	586
DB	763	GGGGAAACCTCAACACCCGGCTTCGGAACCTGACAGAGCAGCAGAGAGTTCACATGCCATCA	704
OY	587	tccctgcaacaacgtcgctcgacagcgcacatggctgcacaaacccgggtttggcgacatctgc	646
DB	703	TCTCTGGCAACACTGTGCTGCGCAGCGCATGTGGCTGGCAGACACCGGGTGGGCGCATCTTCC	644
OY	647	accctgagggaatgcatgtatctgtgtggccagggggccttgggctgtgaagtgcagacca	706
DB	643	ACCCGTGAGGAATGCATGTATCTGTGGCGGCAGGGGGCCTTGGCGTGGAAATGCGAGCCA	584

OY	707	aagaccgagacatcttggaacttgggtgtcgtcacatcccaagaacttcgttcgc	766
Db	583	AGGACCAKGCATCTTTRGATCTGTGGTGTCGACACATCCGAGACTCT -CTTGCT	525
OY	767	gcatacgtagaaaggcccttccttgaggcaccctggaaaggagctcagttgcagtaagc	826
Db	524	GCACTCGTAGAAAGGCCCTTCTCAGGACCCTGGAAGGAGGCGTGCAGTGTGCAGTAAGCG	465
OY	827	tgcataagcttagaaggatattggagcaaccttaccctactggagagagctcggagtctaagc	886
Db	464	TGCATTACAGGTATGAAGAAGATGGCAACTGTACTGTACTGTGAGAGATCTGGAGTTAGACG	405
OY	887	gctcagatatcatcaacaagagacacatgagctgagctaccatccatgttcccctgccagatgaag	946
Db	404	GCTAGATACCATRACANAGAGACCATCAGGCTRACCATCATGATCCCTCCACGATGAG	345
OY	947	atggcccttgtagatlgaccaccaagtlgtltagatcatactgtcgtlaaatccacgaaggc	1006
Db	344	ATGGCCCTGAGATGAGACCCAGTTGTGTAGGATCATCTGCTGTAACTTCCACGAGAGGC	285
OY	1007	ccccagttggtgtccccaagaacttggcgatcagaacctggccaacttgtcttgagcaaggag	1066
Db	284	CCCAGTTGGCTGCCACAGAACCTTGGCATAGGCTGGCCCAACTGTTGCTGAGCAAAGAG	225
OY	1067	ccaaaacatcccttgagatgttcacggccaattgaacgatgcccattaa	1113
Db	224	CCAAAAACATCTCGATGTTCGACGGCACGCTTACAGATGCCCATTTAA	178
RESULT	7		
LOCUS	BE561357	1136 bp	mRNA EST 15-AUG-2000
DEFINITION	601344923F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677764 5',		
ACCESSION	BE561357		
VERSION	BE561357.1	GI:9805077	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1136)		
JOURNAL	NIH-MGC http://mhc.nsl.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-femail.nih.gov		
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov		
	plate: LICM53 row: n column: 05		
	High quality sequence stop: 714.		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:3677764"		
	/clone_lib="NIH_MGC_8"		
	/tissue_type="Burkitt lymphoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: Lymph; Vector: pOTB7; Site_1: XhoI; Site_2:		
	EcoRI; cDNA made by oligo-dT priming. Directionally		
	cloned into EcoRI/XhoI sites using the following 5'		
	adapter: GGCACGAG(G). Size-selected >500bp for average		
	insert size 1.8kb. Library constructed by Ling Hong in		
	the laboratory of Gerald M. Rubin (University of		
	California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies)."*		
BASE COUNT	280 a 298 c 341 g 217 t		

ORIGIN

Query Match 63.5%; Score 706.2; DB 137; Length 1136;
 Best Local Similarity 95.2%; Pred. No. 8.1e-179;
 Matches 770; Conservative 0; Mismatches 13; Indels 26; Gaps 3;

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 1 ggagccatctgtgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 60
 82 agagatctcgtgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 141
 61 agagatctcgtgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 120
 142 gtcgcaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 201
 121 gtcgcaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 180
 202 acagagcaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 261
 181 acagagcaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 240
 262 agagatctcgtgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 321
 241 agagatctcgtgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 276
 322 gtcgcaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 381
 277 gtcgcaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 336
 382 cctcagatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 441
 337 cctcagatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 396
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 622 gtcgcaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 680
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 681 gtcgcaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 740
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 741 gtcgcaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 800
 697 gtcgcaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 756
 801 agagatctcgtgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 828
 757 agagatctcgtgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 785

RESULT 8
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 LOCUS AL516000 LTI.NFL011.NBC1 Homo sapiens cDNA clone CSDDA005Yc03 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL516000
 VERSION AL516000.1 GI:12779493
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 878)
 AUTHORS Li, W.B., Gruber, C., Jesssee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

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 /db_xref="taxon:9606"
 /clone="CSDDA005Yc03"
 /clone_1id="LTI.NFL011.NBC1"
 /sex="male"
 /tissue="neuroblastoma cells"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"
 BASE COUNT 200 a 235 c 264 g 173 t 6 others
 ORIGIN

Query Match 62.7%; Score 698.2; DB 105; Length 878;
 Best Local Similarity 94.3%; Pred. No. 1.1e-176;
 Matches 746; Conservative 4; Mismatches 2; Indels 39; Gaps 1;

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 174 gcaattgtaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 233
 187 gcaattgtaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 246
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 414 tcttggaagaaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 473
 427 tcttggaagaaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 486
 474 aagagcaacatctgtaacgcaatgcygctgcaacgcyggaagaaacagcccaagatg 533
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Db	607	AACACTGCTGCGAGGCATGAGCTGCGACAAACCGG-----	AU132868	812 bp	mRNA	EST	24-OCT-2000						
Qy	654	ggaatgcatgtatctgtgtggccaggggcttgggctgtgaagtgcagccaaagaccca	AU132868	NT2RP4	Homo sapiens	CDNA clone	NT2RP4000750 5', mRNA						
Db	644	-----GTTGGGGGCAAGGGGGCCCTTGGGCGTGGAAGTGCAGGCAAGGACCA	AU132868	1	GI:10993407	EST							
Qy	714	ggacatcttgatctgtgtgggtgtgtcttcacagatccgaagctcgtcttgatctgc	AU132868	812 bp	mRNA	EST	24-OCT-2000						
Db	668	GGACATCTTGGATCTGGGTGGGGTGCTCTACAGATCCGAGACTCTGCTTCCTGATGCG	AU132868	NT2RP4	Homo sapiens	CDNA clone	NT2RP4000750 5', mRNA						
Qy	774	tgaaaggccttccttcgaagcacccttgaagaggagctcagttgtcccaagtcgctgcatac	AU132868	812 bp	mRNA	EST	24-OCT-2000						
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Qy	834	agcatatgaagatgtggcgaactgttacctgactgtggaagatctgtgaagctagaagctcaga	AU132868	812 bp	mRNA	EST	24-OCT-2000						
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VERSION	AU132868	NT2RP4	Homo sapiens	CDNA clone	NT2RP4000750 5', mRNA								
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Db	157	GAAAGAAACAGCC	CAAGATGAGTAGTGAATTCGCCGTG	GCTACCCGACAGCAGCTTGCT	216
Qy	121	cgcatacagaag	gagatgctgtgtgacacatltgaagc	ctcgtacccctgacctgagctt	180
Db	217	GCCATACAGACGC	AGAGTGCTGCAACATTTGAAGCCT	CTGTACCTTGCCCTGCAGTTT	276
Qy	181	gaatcatgtgc	atgtgtccacacaggggacaagatctt	gtatctacgtcactctcctaagtt	240
Db	277	GAAATCATTTGCT	ATGTCTCCACCACAGGGACAGATTT	CTTGATACGTCACTCTTAAGATT	336
Qy	241	ggaagaaagc	gtlttlaaccaaggagctltgacac	tgcccttggagaaagatgagtgagc	300
Db	337	GGAGAGAAAGC	CTGTTTACCAAGAGAGCTTGAAAT	CGCCTGGACAGAAATGAATGGAC	396
Qy	301	ctgtgttctact	ctcttgaaggacctgcccactgtgtc	ttctcctctgcttcaacatgga	360
Db	397	CTGGTTGTTTCA	CTCTTGTGAAGACCTGCCCACAT	GTGCTCTCCCTGACCTTCCATCGGA	456
Qy	361	ggcactcgaag	cgggaaacacccatgatgtgtgtc	ttcttccaccacaatlttgag	420
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Qy	541	acccgagctc	ggaagctgtagcagcagcagagatlc	agtgccatcatcccttgcacaagct	600
Db	637	ACCCGGCTTC	GGAAAGCTGGACAGACAGAGAGTT	CAAGTCAAGTCAATCTCTGGCAACAGCT	696
Qy	601	ggcctgcagc	gcatgtggtgtgcacaaaccggtt	tggtgcagatcctgtcaccccttg	659
Db	697	GGCCTGACAG	CGATGGGCGTGCACAAACGGG	GTGGGAGCATCTGACACCTCGAGGAATG	756
Qy	660	catgtatctgt	gtggccagggggtctgtggctgtg	agatgtcgagcaagagaccagga	716
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DEFINITION				mRNA sequence.	
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VERSION	AL579416.1				
KEYWORDS				EST.	
SOURCE			human.		
ORGANISM			Homo sapiens		
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE			1 (bases 1 to 838)		
JOURNAL			Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		
COMMENT			Full-length cDNA libraries and normalization		
			Unpublished (2001)		
			Contact: Genoscope		
			Genoscope - Centre National de Sequencage		
			BP 191 91006 EVRY cedex - France		
			Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.		
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			/db_xref="taxon:9606"		
			/clone="CSODH004P13"		

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (tLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution
Information can be found through the I.M.A.G.E. Consortium/tLNL at: Image.lnl.gov
Plate: BLCH353 row: m column: 13
High quality sequence step: 723

FEATURES	Location/Qualifiers
source	1. .1087

BASE COUNT	270 a	291 c	345 g	181 t
ORIGIN				

Query Match	59.1%	Score	657.8	DB	137	Length	1087
Best Local Similarity	92.4%	Pred. NO.	8e-166				
Matches	725	Conservative	0	Mismatches	57	Indels	3
						Gaps	3

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Db	143	GAAGAAAAACACCCCAAGAGTAGAGTATTCGCTGGGTACCCCAAGAGCACCTTGCT	202
OY	121	cgaatacagaagcgacatgctgtgtgtgacaacatttgaaagcctctgtacccctggcctgactt	180
Db	203	CGCATACAGACGGACAGTGTGTGTGGCAACATTGAAGCCTGTACCTGGCCTCACTTT	262
OY	181	gaaaatcatctgtatgtccacacagagggaacaagatctctgatactgcactctctaagat	240
Db	263	GAATCATTTGCTATGTCACACACAGGGGACAGATGTTGTTGATGTGCATCTCTAATAAT	322
OY	241	ggaagaagaaacgcgtcttaccaaagagcttgaaatctccctcgagagaagaatgaaatgac	300
Db	323	GGAGAGAAAAACCGTGTATTACCAAGAGACTTGAACATCCCTCGGAGAAATGAAGTGGAC	382
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Db	383	CTGGTTTTCACCTCTTGAAAGAGACCTCCACACTGTGCTTCTCTCGGCTTCACCATGGA	442
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Db	443	GCCATCTGCAAGCGGGAAAAACCTCATGATGCTGTGTCTTTTACCCAAATTTGTGTGG	502
OY	421	aagaaccttagaaacccctgccaagagaagatgtgtgtggaacacagctccctctgcgaagaca	480
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OY	481	ggccaaagtctgaaagaaagtctccgcgcatctggaagtctcaggagtatctggggaaacctaac	540
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Db	623	ACCCGCGTTGGAGAGCTGGAGACAGACAGATGTTCAAGTGCATCATCTGTGGCAACAGC	682
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Db	683	TGGCGTTGACGGGCATGGGCTGGCACAAAGGGGTGGGGACAGATCCTTGCACACTGAGGAAT	74.2
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Db	743	GGCTGTGTTGGTGGTGGG-CAGAGGGGCGCTTTGGGCGTTTGGAATGGGAGGCAAGACCCGGCT	80.1
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Db	802	TCTGGGTTGTGGGGGCGGGCGGAACCGAGAACCCGGTCCGGGGCTCGCTGAAGGCGCTCTGA	86.1
Qy	779	ggagcc 783	
Db	862	GGCCC 866	

RESULT 14	AL520223	908 bp	MRNA	EST	13-FEB-2001
LOCUS	AL520223	LRT_NRL004_NBC2	Homo sapiens cDNA clone	CS0DB006Y103	5
DEFINITION	p12m, mRNA sequence.				
ACCESSION	AL520223				
VERSION	AL520223.1	GI:12783716			
KEYWORDS	EST.				
SOURCE	human.				

REFERENCE	1 (bases 1 to 908)
AUTHORS	Li, W. B., Gruber, C., Jesse, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope

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FEATURES
location/Qualifiers
1. .908
source

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BASE COUNT	208 a	245 c	269 g	183 t	3 others
ORIGIN					

Query Match	58.8%	Score 654.6	DB 105	Length 908
Best Local Similarity	99.3%	Pred. No. 5.Se-165		
Matches 676; Conservative	2;	Mismatches 1;	Indels 2;	Gaps 2;

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QY	120	tcgacatacagacgagacagtctgctggtagaacatttgaagacctctgaacctggcctgcagtc	179
	290	tcgacatacagacgagacagtctgctggtagaacatttgaagacctctgaacctggcctgcagtc	349
QY	180	tgaatcatctgcctctgtgccacacagagggaacaagaattctgcatactacactctcctaagat	239
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Oy 240 tggagagaaagccgtttaccagaagcttgaaacatccccctggagaaagaaatgaatgga 299
Db 410 TGGAGAGAAAGCCGTGTTTCCAGAGACCTTGAAATGCTGCTGGAGAAATGAAGTGA 469
Oy 300 cctggtgttcaactccttgaaagacctgcccactgtgtcttccctgtgttaccatcgg 359
Db 470 CCGTGTGTTCACTCCTTGAAGGACCTGCCACTGTGCTCCTCCTGCTTACCATCGG 529
Oy 360 agccatctgcaagcgaggaaacccatcatgatgtgtgtcttcccaaaaattgttgg 419
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Oy 420 gaagacccttaagaaaccgcaagaagaatgtgtgtggaaacacactccctccgaaagc 479
Db 550 GAAGACCCCTAGAAACCTGTGCCAGAGAAGATGTGTGGGAA-CAGCTCCCTGTCCGAAGAC 648
Oy 480 agcccaagctgcaagaagattcccgacatctgagatcaggaatctcgaggaaacccaa 539
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Db 768 TGGCTTGAGGCCATGGCTGGCAACCGGGTGGGCAAGTCTGACCTCGAGGAAGG 827
Oy 660 catgatctgtgagcgaggggagcttgagcggtggaatgagcgaagaagacagacat 719
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Db 888 CTTCGATCTGTGTGGGTGTGCK 908

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LOCUS 602240467P1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4328848 5',
DEFINITION mRNA sequence.
BF971877
ACCESSION BF971877.1 GI:12339092
VERSION BF971877.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 970)
NIH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-riemail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M1189 row: f column: 17
High quality sequence stop: 724.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4328848"
/clone_11b="NIH_MGC_46"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"

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/note="Organ: uterus; Vector: pOTB7; Site.1: XhoI; Site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the Laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 244 a 262 c 296 g 168 t
ORIGIN

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Query Match 58.5% Score 651; DB 172; Length 970;
Best Local Similarity 94.8%; Pred. No. 5.2e-164;
Matches 716; Conservative 0; Mismatches 35; Indels 4; Gaps 4;

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Oy 1 cacacagcctacttcccaagcgagccatgtctgttaacggaatcgctgcaacggcg 60
Db 110 CACACAGCCTACTTTCCAAGCGGAGCCATGTCTGTAAAGCAATGCGGCTTCACAGCGCG 169
Oy 61 gaagaaacacgcccagaagatgagatgaltcgcgtgggtaccgcaagaagcagctgct 120
Db 170 GAAGAAACAGGCCCAAGATGAGATGATTCGCGTGGTACCCGCAAGACGACCTTGCT 229
Oy 121 cgcatacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
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Oy 181 gaatcatgtcatgttcccaacagggagcaagatctcttgaactgacatcctcctaagt 240
Db 290 GAATCATTTGCTATGTCCACACAGGGAGCAAGATTTCTTGATCTGCACTCTTAAGATT 349
Oy 241 ggaagaaagccgtgttcaacagagcttgacatgcccctggagaaagatgaatgagc 300
Db 350 GGAGAAAGCCCTGTTACAGAGAGCTTGAACATGCCCTGAGAAAGATGAATGAGC 409
Oy 301 ctggtgttcaactccttgaaagacctgcccactgtgtcttccctcgtgttaccatcga 360
Db 410 CTGgtgttCACTCTTGAAAGACCTGCCACTGtgtCTTCTGTGCTTCAACATCGGA 469
Oy 361 gccatctgcaagcggaacacccatcatgatgtgtgttcttccaccaaatltgtgg 420
Db 470 GCCATCTGCAACGGGAAACCCCTCATGATGCTGTGTCTTTACCCCAAAATTTGTGGG 529
Oy 421 aagacccttaagaaacccctgcagaagaagtgtgtgtggaacacagctccctcgaaagca 480
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Db 590 G-CCAGCTGCAAGAAAGTTCCCGCATCTGAGTTCAGAGATATCCGGGGAACCTTCAAC 648
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Db 649 ACCCGGCTTCGGAAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 708
Oy 600 tggcctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 659
Db 709 TGGGCTGCGAGCCATGCGCTGCGCACAMC-GGTGGGCGAGATCTGMAACCTCGAGCAATG 767
Oy 660 catgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 719
Db 768 CCGTATGCTGTGGGCCA-GGGGCTGGGCGTTGTGAATGCGAGCCAGGACCGAGACA 826
Oy 720 ctggaatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 754
Db 827 TTTGGGACACGGGGGAGTGTGACCAACCCGAAA 861

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Search completed: October 6, 2001, 19:05:09
Job time: 5237 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 17:39:53 ; Search time 90.47 Seconds
(without alignments)
2328,985 Million cell updates/sec

Title: US-09-601-138-12

Perfect score: 1113
Sequence: 1 cacacagccacttcccaag.....aatgacagatgcccatata 1113

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : Issued Patents_NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	41.6	3.7	729	1	US-08-599-480-3 Sequence 3, Appl
C 2	36.2	3.3	290	1	US-08-030-731A-41 Sequence 41, Appl
C 3	36.2	3.3	290	1	US-08-030-731A-42 Sequence 42, Appl
C 4	36.2	3.3	304	1	US-07-696-551B-12 Sequence 12, Appl
C 5	35.6	3.2	7218	1	US-08-232-463-14 Sequence 14, Appl
C 6	34.8	3.1	1889	2	US-08-946-241B-1 Sequence 1, Appl
C 7	34.8	3.1	1889	2	US-08-946-241B-8 Sequence 8, Appl
C 8	34.8	3.1	1889	3	US-09-309-053-1 Sequence 1, Appl
C 9	34.8	3.1	1889	3	US-09-309-053-8 Sequence 8, Appl
C 10	34.4	3.1	2502	1	US-08-073-384C-7 Sequence 7, Appl
C 11	34.4	3.1	2502	1	US-08-254-359A-7 Sequence 7, Appl
C 12	34.4	3.1	2502	1	US-08-483-043-7 Sequence 7, Appl
C 13	34.4	3.1	2502	1	US-08-481-238-7 Sequence 7, Appl
C 14	34.4	3.1	2502	2	US-08-471-066B-7 Sequence 7, Appl
C 15	34.4	3.1	2502	2	US-08-484-956-7 Sequence 7, Appl
C 16	34.4	3.1	2502	2	US-08-757-653-7 Sequence 7, Appl
C 17	34.4	3.1	2502	2	US-08-599-491-7 Sequence 7, Appl
C 18	34.4	3.1	2502	2	US-08-756-386-7 Sequence 7, Appl
C 19	34.4	3.1	2502	2	US-08-823-516-7 Sequence 7, Appl
C 20	34.4	3.1	2502	3	US-08-882-853A-7 Sequence 7, Appl
C 21	34.4	3.1	2502	3	US-08-759-038-7 Sequence 7, Appl
C 22	34.4	3.1	2502	3	US-08-758-314-7 Sequence 7, Appl
C 23	34.2	3.1	510	1	US-07-918-953-7 Sequence 7, Appl
C 24	34.2	3.1	510	1	US-08-081-661-7 Sequence 7, Appl
C 25	34.2	3.1	729	4	US-09-140-804-10 Sequence 10, Appl
C 26	34.2	3.1	2793	1	US-08-209-747-1 Sequence 1, Appl
C 27	34.2	3.1	2793	1	US-08-458-298-1 Sequence 1, Appl

28	33.6	3.0	2121	4	US-09-358-683-1 Sequence 1, Appl
29	33.6	3.0	2276	1	US-08-202-389-11 Sequence 11, Appl
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32	33.6	3.0	2790	2	US-08-448-250-4 Sequence 4, Appl
33	33.4	3.0	359	3	US-08-589-028-3 Sequence 3, Appl
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C 36	33.4	3.0	11219	1	US-07-642-734C-1 Sequence 1, Appl
C 37	33.4	3.0	11219	3	US-08-439-009A-1 Sequence 1, Appl
C 38	33.4	3.0	44377	2	US-08-804-227C-7 Sequence 7, Appl
C 39	33.4	3.0	44377	2	US-08-804-198-1 Sequence 1, Appl
C 40	33.2	3.0	1201	6	5252556-2 Patent No. 5252556
C 41	33	3.0	281	1	US-07-764-655D-12 Sequence 12, Appl
C 42	33	3.0	281	1	US-07-764-655D-13 Sequence 13, Appl
C 43	33	3.0	281	6	5514646-1 Patent No. 5514646
C 44	33	3.0	3579	1	US-08-674-168-15 Sequence 15, Appl
C 45	33	3.0	3579	3	US-08-985-908-18 Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-599-480-3/C

Sequence 3, Application US/08599480

Patent No. 5753459

GENERAL INFORMATION:

APPLICANT: Bianco, David R.

APPLICANT: Miller, James N.

APPLICANT: Lovett, Michael A.

APPLICANT: Champion, Cheryl I.

APPLICANT: Tempst, Paul J.

TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF A

RARE OUTR MEMBRANE PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSER: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: California

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/599,480

FILING DATE: 23-JAN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Leart, June M.

REGISTRATION NUMBER: 31,238

REFERENCE/DOCKET NUMBER: 07419/018001 (CIP of 016001)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 678-5070

TELEFAX: (619) 678-5099

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 729 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:

CLONE: TROMP2

FEATURE:

NAME/KEY: CDS

LOCATION: 1..726

US-08-599-480-3

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Best Local Similarity	47.3%	Pred. No. 0.0076		
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QY 314	ccttgaagagacctgtgcacacctgtgcttcctccctgcgttcaacatacggagacacatcgaagc	373		
Db 248	CCTTCCACACGAGACCCGCCCATCGCACCCGCTGTGGCATGCTCCGAAATTACTTGAAGATA	189		
QY 374	gggaanaaccctcaatgatgtctgtg 397			
Db 188	GGGAAGCCCTTGTGTATGTAACCTTG 165			

RESULT 2
 US-08-030-731A-41
 : Sequence 41, Application US/08030731A
 Patent No. 5426036
 GENERAL INFORMATION:
 APPLICANT: Koller, Klaus-Peter
 APPLICANT: Rless, Guenther Johannes
 APPLICANT: Uhlmann, Eugen
 APPLICANT: Wallmeyer, Holger
 TITLE OF INVENTION: Processes for the Preparation of Foreign
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flinnegat, Henderson, Farabow, Garrett &
 ADDRESSER: Dunner
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/030,731A
 FILING DATE: 12-MAR-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/189,840
 FILING DATE: 03-MAY-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/430,622
 FILING DATE: 01-NOV-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/687,610
 FILING DATE: 19-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/735,757
 FILING DATE: 29-JUL-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 37 14 866.4
 FILING DATE: 05-MAY-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 38 37 273.8
 FILING DATE: 03-NOV-1988

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1      PRIOR APPLICATION DATA:
2      APPLICATION NUMBER:  DE P 39 27 449.7
3      FILING DATE: 19-AUG-1989
4      PRIOR APPLICATION DATA:
5      APPLICATION NUMBER:  DE P 40 12 818.0
6      FILING DATE: 21-APR-1990
7      ATTORNEY/AGENT INFORMATION:
8      NAME:  Kirschner Michael K.
9      REGISTRATION NUMBER:  34,851
10     REFERENCE/DOCKET NUMBER: 02481-0593-020000
11     TELECOMMUNICATION INFORMATION:
12     TELEPHONE: 202-408-4000
13     TELEFAX: 202-408-4400
14     INFORMATION FOR SEQ ID NO: 41:
15     SEQUENCE CHARACTERISTICS:
16     LENGTH: 290 base pairs
17     TYPE: nucleic acid
18     STRANDEDNESS: both
19     TOPOLOGY: linear
20     MOLECULE TYPE:  DNA (genomic)
21     US-08-030-731A-41

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Matches	116;	Conservative	0;	Mismatches	133;	Indels	0;
				Gaps			0

[illegible]

RESULT 3
 US-08-030-731A-42/C
 ; Sequence 42, Application US/08030731A
 ; Patent No. 5426036
 ; GENERAL INFORMATION:
 ; APPLICANT: Koller, Klaus-Peter
 ; APPLICANT: Riess, Guenther Johannes
 ; APPLICANT: Uhlmann, Eugen
 ; APPLICANT: Walmeier, Holger
 ; TITLE OF INVENTION: Processes for the Preparation of Foreign
 ; TITLE OF INVENTION: Proteins in Streptomycetes
 ; NUMBER OF SEQUENCES: 48
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flinagan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,731A
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/189,840
FILING DATE: 03-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/430,622
FILING DATE: 01-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/687,610
FILING DATE: 19-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,757
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 37 14 866.4
FILING DATE: 05-MAY-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 38 37 273.8
FILING DATE: 03-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 39 27 449.7
FILING DATE: 19-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 12 818.0
FILING DATE: 21-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kirschner Michael K.
REGISTRATION NUMBER: 34,851
REFERENCE/DOCKET NUMBER: 02481-0593-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
FEATURE:
NAME/KEY: misc.feature
LOCATION: 5..290
OTHER INFORMATION: /note="Sequence ID No. 5426036 42 is
OTHER INFORMATION: complementary to Sequence ID No. 5426036 41 at positions
OTHER INFORMATION: 5-290 of Sequence ID No. 5426036 41."
US-08-030-731A-42

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Query Match          3.3%; Score 36.2; DB 1; Length 290;
Best Local Similarity 46.6%; Pred. No. 0.19;
Matches 116; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

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DB 275 ACCAGCACCTGTGGGTGCTCCACCTAGTGAAGCTCTCTACCTGTGCTGGGAGGAG 216

QY 623 acaacgggttggcagatctctgacccctgaggaatgcatgltgctgtggccaagg 682
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QY 683 ccttggcgtgagtgatcgagccaaggaagacatcttgatctgtgtgtgtgtgc 742
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DB 155 AGCTGGGCGGGGGCCCTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 96

QY 743 acgatcccgagactctgcttgcgtgcatcgctgaaggcccttcctgaaggcaactgaag 802
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 95 AGAAGCGCGGCAATCTGTGAGCAGTGTGACACAGCATCTGCTCCTACCACTGGAGA 36

QY 803 gagctgca 811

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DB 35 ACTACTGCA 27
|||||
RESULT 4
US-07-696-551B-12
Sequence 12, Application US/07696551B
Patent No. 5232841
GENERAL INFORMATION:
APPLICANT: Hashimoto, Tamotsu
APPLICANT: Tsujimura, Atsushi
APPLICANT: Uda, Shigeo
TITLE OF INVENTION: Process for Preparing Peptide
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/PC-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/696,551B
FILING DATE: 19910509
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-122166
FILING DATE: 11-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-334575
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence M. Laylin, Jr.
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 2481-1070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-696-551B-12

Query Match          3.3%; Score 36.2; DB 1; Length 304;
Best Local Similarity 46.6%; Pred. No. 0.19;
Matches 116; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 563 agcagaaggttcagtcgcatcctcctgcaacagctgcaagcgtgagcgtgctgac 622
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DB 43 ACCAGCACCTGTGGGTGCTCCACCTAGTGAAGCTCTCTACCTGTGCTGGGAGGAG 102

QY 623 acaacgggttggcagatctctgacccctgaggaatgcatgltgctgtggccaagg 682
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DB 103 GCTTCTTCTACACACCACCCGAGGAGGAGAGAGACCTCAGGTGGGAGGTGG 162

QY 683 ccttggcgtgagtgatcgagccaaggaagacatcttgatctgtgtgtgtgtgc 742
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DB 163 AGCTGGGCGGGGGCCCTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 222

QY 743 acgatcccgagactctgcttgcgtgcatcgctgaaggcccttcctgaaggcaactgaag 802
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DB 223 AGAAGCGCGGCAATCTGTGAGCAGTGTGACACAGCATCTGCTCCTACCACTGGAGA 282

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ADDRESS: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,384C
FILING DATE: 04-JUN-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FOS-00613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
US-08-073-384C-7

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Query Match 3.1%: Score 34.4; DB 1, Length 2502;
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Qy 611 gcatggagctgagacacacgcgggtctggcagatctcgaacctggaatgatcatgtatgctg 670
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Qy 731 tgggtgtgcctgcagcatccgcgaagactctgtctgctgcatcgctgaaagcg 781
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Db 1472 TGGAAAGCGTGCTCTTTGACGAGCTNNGCGCTTCCCGCATCGCAAGACAGG 1522
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RESULT 11
US-08-254-359A-7
: Sequence 7, Application US/08254359A
: Patent No. 5614402
: GENERAL INFORMATION:
: APPLICANT: DAHLBERG, JAMES E.
: APPLICANT: LYAMICHEV, VICTOR I.
: APPLICANT: BROW, MARY ANN D.
: TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
: TITLE OF INVENTION: DNA POLYMERASE
: NUMBER OF SEQUENCES: 40
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
: STREET: 220 MONTGOMERY STREET, SUITE 2200

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Search completed: October 6, 2001, 17:40:12
Job time: 139 sec

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:      NUMBER OF SEQUENCES: 114
:      CORRESPONDENCE ADDRESS:
:      ADDRESSEE: HAYSTACK, MEDLEN & CARROLL
:      STREET: 220 MONTGOMERY STREET, SUITE 2200
:      CITY: SAN FRANCISCO
:      STATE: CALIFORNIA
:      COUNTRY: UNITED STATES OF AMERICA
:      ZIP: 94104
:      COMPUTER READABLE FORM:
:      MEDIUM TYPE: Floppy disk
:      COMPUTER: IBM PC compatible
:      OPERATING SYSTEM: PC-DOS/MS-DOS
:      SOFTWARE: Patent Release #1.0, Version #1.25
:      CURRENT APPLICATION DATA:
:      APPLICATION NUMBER: US/08/484,956
:      FILING DATE:
:      CLASSIFICATION: 435
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: US 08/402,601
:      FILING DATE: 09-MAR-1995
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: US 08/337,164
:      FILING DATE: 09-NOV-1994
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: US 08/254,359
:      FILING DATE: 06-JUN-1994
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: US 08/073,384
:      FILING DATE: 04-JUN-1993
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: US 07/986,330
:      FILING DATE: 07-DEC-1992
:      ATTORNEY/AGENT INFORMATION:
:      NAME: CARROLL J, PETER G.
:      REGISTRATION NUMBER: 32,837
:      REFERENCE/DOCKET NUMBER: FORS-01801
:      TELECOMMUNICATION INFORMATION:
:      TELEPHONE: (415) 705-8410
:      TELEFAX: (415) 397-8338
:      INFORMATION FOR SEQ ID NO: 7:
:      SEQUENCE CHARACTERISTICS:
:      LENGTH: 2502 base pairs
:      TYPE: nucleic acid
:      STRANDEDNESS: single
:      TOPOLOGY: linear
:      MOLECULE TYPE: DNA (genomic)
:      US-08-484-956-7

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Query Match      3.1%; Score 34.4; DB 2; Length 2502;
Best Local Similarity 44.0%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

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QY 611 gcatgggtctgcaacaacccggttgggagatcctgcaacctgaggaatgatgtatgctg 670
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QY 731 tgggtgtgtgcaagatcccgagactctgcttgctgcatcgatgaaagg 781
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Db 1472 TGGAAAGGGTGTCTTTCAGACGACTNGGCTTCGCCCATCGCAAGACGG 1522

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FT /note="silent mutation"
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 PN W0937325-A2.
 PD 29-JUL-1999.
 XX
 PF 27-JAN-1999; 99WO-DK00040.
 XX
 PR 30-DEC-1998; 98DK-000174B.
 PR 27-JAN-1998; 98DK-0000112.
 XX
 PA (HEME-) HEMEBIOTEC AS.
 PI Pogh J, Gellerfors P;
 XX WPI: 1999-478987/40.
 DR P-PSDB; AAY06611.
 XX
 PT Treatment of acute intermittent porphyria and other porphyric
 PT diseases using an enzyme belonging to the haem biosynthetic pathway
 XX
 PS Claim 36; Page 91; 100pp; English.
 XX
 CC This is the nucleotide sequence of human PBGD clone 1.1 coding for
 CC an erythropoietic expressed form of porphobilinogen deaminase
 CC (PBGD, see AAY06611). PBGD catalyses the rate-limiting step of the
 CC haem biosynthetic pathway. cDNA was cloned from spleen, bone
 CC marrow, lymph node, lung, whole brain and adipose tissue using a
 CC nested PCR strategy. 8 PBGD clones were sequenced (see AAX87630 and
 CC AAX87632-38). Clone 1.1, from spleen cDNA, has 5 changes from the
 CC previously published sequence but represents the most prevalent
 CC 'wild-type' allele in the population. Mutation of the PBGD gene is
 CC associated with the autosomal dominant disorder acute intermittent
 CC porphyria (AIP). A claimed method of treating a patient having a
 CC mutation in the PBGD gene comprises using a human PBGD cDNA
 CC sequence of either non-erythropoietic form (see AAX87631) or
 CC erythropoietic form (especially the present sequence) according
 CC to the tissue in which PBGD should be expressed, and transfection
 CC of the patient with the relevant cDNA. Gene therapy treatment of
 CC patients with AIP by a correction of one of the specific point
 CC mutations identified as causing the disease by use of chimera-plasty
 CC gene repair is also claimed. Other enzymes involved in the haem
 CC biosynthetic pathway can also be used to treat various porphyrias.
 XX
 SO Sequence 1035 BP; 250 A; 271 C; 302 G; 212 T; 0 other:

Query Match 100.0%; Score 1035; DB 20; Length 1035;
 Best Local Similarity 100.0%; Pred. No. 2e-279;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 gtggtgcaacaatcgaaagctctaacctgctgacgttgaataatcgtatgtcc 120
 OY 121 accacaggggaagaatctctgatactgacactctctaagatgtgagagaaagctgttt 180
 DB 121 accacaggggaagaatctctgatactgacactctctaagatgtgagagaaagctgttt 180
 OY 181 accaagagcttgaacatgcccctggagagaaatgaagtgtgactgtgttccactcttg 240
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DB 301 aacctcatgactgtgtcttcaaccacaattgttggaagaccctagaaccctg 360
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 DB 661 ctgcagatcccgagacctcgtctcgtcgcacatcgctgaaaggcccttcagagcaccctg 720
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 DB 721 gaagagagctcagatgtgtcagatgacgtgtatagatgaagagatggagacatctgtac 780
 OY 781 ctgactgagagatctgagatcagacggtccacagatacacaagaagagacatcagagct 840
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 DB 841 accatccatctccctcggccagatgaagatgacctgtgagatgaccccaatctgttaggc 900
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 OY 1021 aacgatgccattaa 1035
 DB 1021 aacgatgccattaa 1035

RESULT 2
 AAF72848
 ID AAF72848 standard; DNA: 1035 BP.
 XX
 AC AAF72848;
 DT 24-APR-2001 (first entry)
 XX
 DE Erythropoietic form PBGD 1.1.
 XX
 KW Heme biosynthetic pathway; gene therapy: AIP; ALA;
 KW delta-aminolevulinic acid; deficient porphyria; ADP;
 KW porphyria cutanea tarda; PCT; hereditary coproporphyria; HCP;
 KW hereditary erythropoietic protoporphyria; VP;
 KW congenital erythropoietic porphyria; CEP;
 KW erythropoietic protoporphyria; EPP;
 KW hepatoerythropoietic porphyria; HEP; ds.
 XX Homo sapiens.
 OS
 XX
 PN W0200107065-A2.

PD 01-FEB-2001.
XX
PF 27-JUL-2000; 2000MO-DK00425.
XX
PR 27-JUL-1999; 99DK-0001071.
PR 19-APR-2000; 2000DK-0000667.
XX
PA (HEME-) HEMEBIOTEC AS.
XX
PI Gellerfors P, Fogh J;
XX WPI, 2001-159639/16.
XX
DR
XX
PT Treatment or prevention of porphyria, by enzyme replacement or gene
PT therapy for correction of mutations, particularly in the
PT porphobilinogen deaminase gene
PS
PS Claim 33; Page 200; 207pp; English.
XX
XX The present invention relates to treatment or prevention of a
CC disease caused by deficiency of at least one enzyme of the
CC heme biosynthetic pathway by administering at least one catalyst,
CC optionally combined with gene therapy of the relevant mutation.
CC The invention is useful for treating and/or preventing ALP, ALA
CC (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
CC cutanea tarda (PCT), hereditary coproporphyria (HCP), harderoporphyria
CC (HDP), variegate porphyria (VP), congenital erythropoietic porphyria
CC (CEP), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
CC porphyria (HEP).
XX
SQ Sequence 1035 BP; 250 A; 271 C; 302 G; 212 T; 0 other:

Query Match 100.0%; Score 1035; DB 22; Length 1035;
Best Local Similarity 100.0%; Pred. No. 2e-279;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 601 ggggacctgggctggaagctgcagaccgaagacagacatcttgatctgtgtggctg 660
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Db 1021 aacgagccccattaa 1035

RESULT 3
AAx87631
ID AAx87631 standard; cDNA; 1113 BP.
XX
AC AAx87631;
XX
DT 26-OCT-1999 (first entry)
XX
DE Human non-erythroid porphobilinogen deaminase clone 1.1.1.
XX
KW Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
KW porphyria cutanea tarda; hereditary coproporphyria;
KW harderoporphyria; congenital erythropoietic porphyria;
KW variegate porphyria; erythropoietic protoporphyria;
KW hepatoerythropoietic porphyria; acute intermittent porphyria;
KW gene therapy; enzyme replacement therapy; ds.
XX
OS Homo sapiens.
XX
PN MO9937325-A2.
XX
PD 29-JUL-1999.
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PF 27-JAN-1999; 99MO-DK00040.
XX
PR 30-DEC-1998; 98DK-0001748.
PR 27-JAN-1998; 98DK-0000112.
XX
PA (HEME-) HEMEBIOTEC AS.
XX
PI Fogh J, Gellerfors P;
XX
DR WPI, 1999-478987/40.
XX
PT Treatment of acute intermittent porphyria and other porphyric
PT diseases using an enzyme belonging to the haem biosynthetic pathway

XX Claim 36; Page 99-100; 100pp; English.
 PS This is the nucleotide sequence of human PBGD clone 1.1.1 coding
 CC for a constitutive form of porphobilinogen deaminase (PBGD).
 CC This enzyme catalyses the third, rate-limiting step of the haem
 CC biosynthetic pathway. Mutation of the PBGD gene is associated
 CC with the autosomal dominant disorder acute intermittent porphyria
 CC (AIP). A claimed method of treating a patient having a mutation
 CC in the PBGD gene comprises using a human PBGD cDNA sequence of
 CC either the present, non-erythropoietic form or an erythropoietic
 CC form (see AA87630) according to the tissue in which PBGD should be
 CC expressed, and transfection of the patient with the relevant cDNA.
 CC Gene therapy treatment of patients with AIP by a correction of one
 CC of the specific point mutations identified as causing the disease
 CC by use of chimeraplasty gene repair is also claimed. Other enzymes
 CC involved in the haem biosynthetic pathway can also be used to treat
 CC various porphyrias.
 CC
 SC Sequence 1113 BP; 274 A; 294 C; 323 G; 222 T; 0 other;

Query Match 100.0%; Score 1035; DB 20; Length 1113;

Best Local Similarity 100.0%; Pred. No. 2,1e-279;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 gtggtgcaacattgaaggcctgacccctgagcctgctgaaataatgctatgcc 120
 Db 139 gtggtgcaacattgaaggcctgacccctgagcctgctgaaataatgctatgcc 198
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 Db 379 aacctcatalgtcgtgtctcttccaccanaattgtgtggaagaccctagaaccctg 438
 QY 361 ccaagaaagagtggtggtggaacagcctctgagaaagagccagctgcaagaaag 420
 Db 439 ccaagaaagagtggtggtggaacagcctctgagaaagagccagctgcaagaaag 498
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 QY 481 gacgagacgagcagagttcagtgccatcctcgtgcaaacagctgagcctgcaagcgatgggc 540
 Db 559 gacgagacgagcagagttcagtgccatcctcgtgcaaacagctgagcctgcaagcgatgggc 618
 QY 541 tggcacaacacgggtctggcagagatctcgtcaccttgaggaatgcatgctgctggccag 600
 Db 619 tggcacaacacgggtctggcagagatctcgtcaccttgaggaatgcatgctgctggccag 678
 QY 601 ggggccttggtggtgagagtgcaagcagaagcagagcacttgatctgtgtgtgtg 660
 Db 679 ggggccttggtggtgagagtgcaagcagaagcagagcacttgatctgtgtgtgtg 738
 QY 661 ctgcaagatcccgagactctgtctgctgcatcgctgaaaggccttccctgagcacctg 720
 Db 739 ctgcaagatcccgagactctgtctgctgcatcgctgaaaggccttccctgagcacctg 798

QY 721 gaagagagctgcaagtgtgtccagtagcgtgtgcatagactatgaagatgagcactgtac 780
 Db 799 gaagagagctgcaagtgtgtccagtagcgtgtgcatagactatgaagatgagcactgtac 858
 QY 781 ctgacttgagagagctgtgagcttagacggtcagatagacatacagagacacatgagct 840
 Db 859 ctgacttgagagagctgtgagcttagacggtcagatagacatacagagacacatgagct 918
 QY 841 accatccatgtctcctgcccagatgaagaatgagccttgagagatgaccccaagtgtgtaggc 900
 Db 919 accatccatgtctcctgcccagatgaagaatgagccttgagagatgaccccaagtgtgtaggc 978
 QY 901 atccatgtctgtaaatctccacagagagccagctgtgctgcccaagacttgagctcagc 960
 Db 979 atccatgtctgtaaatctccacagagagccagctgtgctgcccaagacttgagctcagc 1038
 QY 961 ctggccaactgtgtgtgtgagcaaaagagcacaacacccctgagatgtgcaagcaatg 1020
 Db 1039 ctggccaactgtgtgtgtgagcaaaagagcacaacacccctgagatgtgcaagcaatg 1098
 QY 1021 aacgattgccattaa 1035
 Db 1099 aacgattgccattaa 1113

RESULT 4

AAE72849
 ID AAE72849 standard; DNA: 1113 BP.

AAE72849;

24-APR-2001 (first entry)

Non-erythropoietic form PBGD 1.2.

KW Heme biosynthetic pathway; gene therapy; AIP; ALA;
 KW delta-aminolevulinic acid; deficient porphyria; ADP;
 KW porphyria cutanea tarda; PCT; hereditary coproporphyria; HCP;
 KW haderoporphyria; HBP; variegata porphyria; VP;
 KW congenital erythropoietic porphyria; CEP;
 KW erythropoietic protoporphyria; EPP;
 KW hepatocerythropoietic porphyria; HEP; ds.

XX Homo sapiens.

OS MO200107065-A2.

PN 01-FEB-2001.

XX 27-JUL-2000; 2000MO-DK00425.

XX 27-JUL-1999; 99DK-0001071.

PR 19-APR-2000; 2000DK-0000667.

XX (HEME-) HEMEBIOTEC AS.

PI Gellerfors P, Fogh J;

XX WPI; 2001-159639/16.

PT Treatment or prevention of porphyria, by enzyme replacement or gene

PT therapy for correction of mutations, particularly in the

PT porphobilinogen deaminase gene

PS Claim 33; Page 200; 207pp; English.

CC The present invention relates to treatment or prevention of a
 CC disease caused by deficiency of at least one enzyme of the
 CC heme biosynthetic pathway by administering at least one catalyst,
 CC optionally combined with gene therapy of the relevant mutation.
 CC The invention is useful for treating and/or preventing AIP, ALA
 CC (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria

CC cutanea tarda (PCT), hereditary coproporphyrria (HCP), harderoporphyria
CC (HBP), variegate porphyria (VP), congenital erythropoietic porphyria
CC (CEP), erythropoietic protoporphyria (EPP) and hepatocerythropoietic
CC porphyria (HEP).

SQ Sequence 1113 BP; 274 A; 294 C; 323 G; 222 T; 0 other;

Query Match	100.0%	Score 1035:	DB 22:	Length	1113;			
Best Local Similarity	100.0%;	Pred. No.	2.1e-279;					
Matches 1035;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

QY	1	atgagagatgctgcgcgtgggtatcccccgaagaagcaactctctgacataagagagcaat	60
Dp	79	atgagagatgctgcgcgtgggtatcccccgaagaagcaagctctgacataagagagcaat	138
QY	61	gtggtgcaacaatctgaaagagctctgtaaccccgctgcgtgcagtcttgaaatactatgctatgcc	120
Dp	139	gtggtgcaacaatctgaaagagctctgtaaccccgctgcgtgcagtcttgaaatactatgctatgcc	198
QY	121	acccacaggggagacaagatctctgtgatactctgcaactctctctaaagatttgagagagaaagcctgttt	180
Dp	199	acccacaggggagacaagatctctgtgatactctctctaaagatttgagagagaaagcctgttt	258
QY	181	acccaagagagctctgaaacatgcccgcggagaaagaaatggaagtggacctgtgttctcaactccctg	240
Dp	259	acccaagagagctctgaaacatgcccgcggagaaagaaatggaagtggacctgtgttctcaactccctg	318
QY	241	aaggacactggcccaatctgtgcttccctccctgcgtcttaacactctggagacatctctgcagaagcggtga	300
Dp	319	aaggacactggcccaatctgtgcttccctccctgcgtcttaacactctggagacatctctgcagaagcggtga	378
QY	301	aacctcatgctgctctgtctctctctcaaccccaaaatttgcttgagagagacccctagaagaaacccctg	360
Dp	379	aacctcatgctgctctgtctctctctcaaccccaaaatttgcttgagagagacccctagaagaaacccctg	438
QY	361	ccaaagagaagagtgctgtgtgtgtgtggaacacagctccctctgcgaagagagcccaagctctgcagagagaag	420
Dp	439	ccaaagagaagagtgctgtgtgtgtgtggaacacagctccctctgcgaagagagcccaagctctgcagagagaag	498
QY	421	ttcccgcatctcgaggtcttcagaagagatcttcggtgggaaaccttcacaacccggctcttgaaagctcg	480
Dp	499	ttcccgcatctcgaggtcttcagaagagatcttcggtgggaaaccttcacaacccggctcttgaaagctcg	558
QY	481	gaacagagcaagcgaggtcttcagctgcacatcatctcttgacaacagctctgacctgcagcgcatctgggctc	540
Dp	559	gaacagagcaagcgaggtcttcagctgcacatcatctcttgacaacagctctgacctgcagcgcatctgggctc	618
QY	511	tgcgcaacaacgggtcttggtgcagaaatctctgcacccctgtagaagaaatgcaatgcatctgtctgtgcag	600
Dp	619	tgcgcaacaacgggtcttggtgcagaaatctctgcacccctgtagaagaaatgcaatgcatctgtctgtgcag	678
QY	601	gggggcctctggggtcgtgtggaaggttgagggccaagaagaaatctctgtgatactcggtgtgggttggtg	660
Dp	679	gggggcctctggggtcgtgtggaaggttgagggccaagaagaaatctctgtgatactcggtgtgggttggtg	738
QY	661	ctggaacagatctcccaagaaactctgctcttcagctctgtgatactgccttgaaaggggctctctccagagcaactcg	720
Dp	739	ctggaacagatctcccaagaaactctgctcttcagctctgtgatactgccttgaaaggggctctctccagagcaactcg	798
QY	721	gaagagagagctgacagtgctgtgcagatgacccgtgcatacagctctatgaagagatggggacaactgtac	780
Dp	799	gaagagagagctgacagtgctgtgcagatgacccgtgcatacagctctatgaagagatggggacaactgtac	858
QY	781	ctggaacttggaagaaagctcttggaagctctgaagagctcaagaatgagaaataagaagagacaatgagagct	840
Dp	859	ctggaacttggaagaaagctcttggaagctctgaagagctcaagaatgagaaataagaagagacaatgagagct	918
QY	841	aaccaatccatctgcccctctgcacagatctgaagaaatgagccctctgagagaaatgaaacccaacagctctgtgataagc	900
Dp	919	aaccaatccatctgcccctctgcacagatctgaagaaatgagccctctgagagaaatgaaacccaacagctctgtgataagc	978
QY	901	atcacactgctgtaacaatctcaacagagagccccaagcttggtgcctgcacgaagaacttggtgcatacagc	960

Db 979 ataccctctctgttaacatccacgaaggcccccgttgcgcgcgcacaaatctggcgatccagc 1038

Qy 961 ctggcccaactctgtgtgcgcgaaagaagcgcacaaataatctctgatgttgcacgcgaattg 1020

Db 1039 ctggcgcacactctgttgcgcgagacaaaggacccaaaatactctcctggatgagctgcacgcgaattg 1098

Qy 1021 aacgatgcccatcaa 1035

Db 1099 aacgatgcccatcaa 1113

RESULT 5
 ID AAF72858 standard; DNA: 1260 BP.
 AC AAF72858;
 XX
 XX 24-APR-2001 (first entry)
 DT
 DE (PDGB) DNA.
 KM Gene biosynthetic pathway: gene therapy: ATP; ALA:
 KM delta-aminolevulinic acid; deficient porphyria: ADP;
 KM porphyria cutanea tarda; PCT; hereditary coproporphyria: HCP;
 KM hantroporphyria; HDP; variegate porphyria: VP;
 KM congenital erythropoietic porphyria; CEP;
 KM erythropoietic protoporphyria; EPP;
 KM hepatocerythropoietic porphyria; HEP; ds.
 XX Homo sapiens.
 OS
 XX WO200107065-A2.
 PN
 XX 01-FEB-2001.
 PD
 XX 27-JUL-2000; 2000WO-DK00425.
 PF
 XX 27-JUL-1999; 99DK-0001071.
 PR 19-APR-2000; 2000DK-0000667.
 PR
 XX (HEME-) HEMEBIOTECH AS.
 PA
 XX Gellerfors P, Fogh J;
 PI
 XX WPI: 2001-159639/16.
 DR
 XX
 XX Treatment or prevention of porphyria, by enzyme replacement or gene
 PT therapy for correction of mutations, particularly in the
 PT porphobilinogen deaminase gene -
 XX
 XX Disclosure; Page 205; 207pp; English.
 CC The present invention relates to treatment or prevention of a
 CC disease caused by deficiency of at least one enzyme of the
 CC heme biosynthetic pathway by administering at least one catalyst,
 CC optionally combined with gene therapy of the relevant mutation.
 CC The invention is useful for treating and/or preventing ATP, ALA
 CC (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
 CC cutanea tarda (PCT), hereditary coproporphyria (HCP), hantroporphyria
 CC (HDP), variegate porphyria (VP), congenital erythropoietic porphyria
 CC (CEP), erythropoietic protoporphyria (EPP) and hepatocerythropoietic
 CC porphyria (HEP).
 CC
 XX
 SO Sequence 1260 BP; 309 A; 335 C; 358 G; 258 T; 0 other:

Query Match 100.0%; Score 1035; DB 22; Length 1260;
 Best Local Similarity 100.0%; Pred. No. 2.2e-279;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 atgagagtcattcgcgttggtggtaccgcgaagagccagcttcgcgatacagcggaacgt 60
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Query Match	Score	DB	Length
Best Local Similarity	100.0%	1035	22
Matches 1035; Conservative	100.0%	Precl. No. 2.2e-279;	
	0;	Mismatches	0;
		Indels	0;
		Gaps	0;

QY 1 atgagagtgattcgcgttggtgtaccgcgaagagaccagcttgcgcgcatacagcggaacgt 60
 |||||||

QY 1 atgagagtgatcgcgcgttggtggtaccgcgaagagccagcttgctcgcatacagacgcgacagt 600
|||||

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Db 131 atgagagtgatctcgctggtgtacccgcaagagccagctgtctgcatacagacggaagct 190
Qy 61 gtctgtgcaacaatctgaaagccctcgtatcccttggtccttcagattgaaatcatctatgtcc 120
Db 191 gtctgtgcaacaatctgaaagccctcgtatcccttggtccttcagattgaaatcatctatgtcc 250
Qy 121 accacagggagacaagaattcttgaatctacatctctctaaagattggagagaaagccgtttt 180
Db 251 accacagggagacaagaattcttgaatctacatctctctaaagattggagagaaagccgtttt 310
Qy 181 accacagagacttgaaacaatcctctgagaaagaaatgaaatgagactgtgtgttctaccccttg 240
Db 311 accacagagacttgaaacaatcctctgagaaagaaatgaaatgagactgtgtgttctaccccttg 370
Qy 241 aagagacgtcccaactgtgtcttccctctgtgtctacacatctgagacatctgcagacgggaa 300
Db 371 aagagacgtcccaactgtgtcttccctctgtgtctacacatctgagacatctgcagacgggaa 430
Qy 301 aacctctatgagctgtgtcttcttcaaccataatctgtgtggaaagacccatagaacccttg 360
Db 431 aacctctatgagctgtgtcttcttcaaccataatctgtgtggaaagacccatagaacccttg 490
Qy 361 ccaagagaaagtgctgtgtggaaacagctccctctgagaaagacagctgcagagagaaag 420
Db 491 ccaagagaaagtgctgtgtggaaacagctccctctgagaaagacagctgcagagagaaag 550
Qy 421 ttcctcgatctctgagatctcagagatctcggtggaaacccaacacccggctctcgaaagctg 480
Db 551 ttcctcgatctctgagatctcagagatctcggtggaaacccaacacccggctctcgaaagctg 610
Qy 481 gacagagcagcagagatctcagatctcactcctgcaacagctgagcctgcagagccttgagc 540
Db 611 gacagagcagcagagatctcagatctcactcctgcaacagctgagcctgcagagccttgagc 670
Qy 541 tggcaacaacgggtctggcagaatctctgcacccctgagagaaatgcatgtacgtctgtggccag 600
Db 671 tggcaacaacgggtctggcagaatctctgcacccctgagagaaatgcatgtacgtctgtggccag 730
Qy 601 ggggacctggggctgtggaaagctcggagccaaagacacagacatctctggtatctgtgtgtg 660
Db 731 ggggacctggggctgtggaaagctcggagccaaagacacagacatctctggtatctgtgtgtg 790
Qy 661 ctgcacagatcccgaaacactctctctgcctgcatacgtctgaaagggccctctctgaaagcactg 720
Db 791 ctgcacagatcccgaaacactctctctgcctgcatacgtctgaaagggccctctctgaaagcactg 850
Qy 721 gaaagagagctcagatctgtccagtagccgtgcatacagactagaaagatggagcctgaactgtac 780
Db 851 gaaagagagctcagatctgtccagtagccgtgcatacagactagaaagatggagcctgaactgtac 910
Qy 781 ctgacttgaaagagctctgaaagctctgaagcctcagatagacatacagaagacatgcaagct 840
Db 911 ctgacttgaaagagctctgaaagctctgaagcctcagatagacatacagaagacatgcaagct 970
Qy 841 accatctcactgtccctgcagacatgaaatgagccctctgagagctgagcccaactgtgtacgc 900
Db 971 accatctcactgtccctgcagacatgaaatgagccctctgagagctgagcccaactgtgtacgc 1030
Qy 901 atcaactgtctgaacatctcagagagggcccaagtgtgctgccaaactgtggagacacgc 960
Db 1031 atcaactgtctgaacatctcagagagggcccaagtgtgctgccaaactgtggagacacgc 1090
Qy 961 ctggcacaactgtctgtgagaaagagccaaataatccctggatgtgttcacagcgaacttg 1020
Db 1091 ctggcacaactgtctgtgagaaagagccaaataatccctggatgtgttcacagcgaacttg 1150
Qy 1021 aagagatgcccattaa 1035
Db 1151 aagagatgcccattaa 1165

```

RESULT 6
AAx87639/c

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ID  AAx87639 standard; cDNA; 3988 BP.
XX
AC  AAx87639;
XX
XX  26-OCT-1999 (first entry)
DT
DE  Human porphobilinogen deaminase clone 1.1 in pBluescript SK-.
XX
XX  Porphobilinogen deaminase; human; haem; ALA deficiency porphyrin;
KW  porphyrin cutanea tarda; hereditary coproporphyrin;
KW  hereditary porphyrin; congenital erythropoietic porphyrin;
KW  variegate porphyrin; erythropoietic protoporphyria;
KW  hepatoerythropoietic porphyrin; acute intermittent porphyrin;
KW  gene therapy; enzyme replacement therapy; plasmid pBluescript SK-;
KW  ds.
XX
OS  Homo sapiens.
XX
XX  Key
FH  Location/Qualifiers
FT  complement (1730..696)
FT  CDS
FT  /tag= a
XX
XX  W09937325-A2.
XX
XX  29-JUN-1999.
XX
XX  27-JAN-1999; 99WO-DK00040.
XX
XX  30-DEC-1998; 98DK-0001748.
XX  27-JAN-1998; 98DK-0000112.
XX
XX  (HEME-) HEMEBIOTECH AS.
XX
XX  Fogh J, Gellerfors P;
PI  WPI: 1999-478987/40.
XX  P-PSDB: AAY06611.
XX
XX  Treatment of acute intermittent porphyrin and other porphyric
PT  diseases using an enzyme belonging to the haem biosynthetic pathway
PT
XX
XX  Disclosure; Fig 9a-x; 100pp; English.
XX
XX  This is the nucleotide sequence of human PBGD clone 1.1 (see
CC  AA87630) in plasmid Bluescript SK-, allowing recombinant expression
CC  of porphobilinogen deaminase (PBGD, see AAY06611). PBGD catalyses
CC  the rate-limiting step of the haem biosynthetic pathway. Mutation
CC  of the PBGD gene is associated with the autosomal dominant disorder
CC  acute intermittent porphyrin (AIP). A claimed method of treating a
CC  patient having a mutation in the PBGD gene comprises using a human
CC  PBGD cDNA sequence of either non-erythropoietic form (see AA87631)
CC  or erythropoietic form (especially clone 1.1 cDNA), according to the
CC  tissue in which PBGD should be expressed, and transfection of the
CC  patient with the relevant cDNA. Gene therapy treatment of patients
CC  with AIP by a correction of one of the specific point mutations
CC  identified as causing the disease by use of chimeraplasty gene
CC  repair is also claimed.
XX
XX  Sequence 3988 BP; 918 A; 1056 C; 1000 G; 1014 T; 0 other;
SQ

```

Query Match 100.0%; Score 1035; DB 20; Length 3988;
Best Local Similarity 100.0%; Pred. No. 3.7e-279;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 atgagatgatttcggtgggtaccggaagaagcaggttctgcatacagagcgaagct 60
Db 1730 ATGAGATGATTTCGGTGGGTACCGGAAGAGCCAGCTTCTGCATACAGAGGAGACT 1671
Qy 61 gtgtgtgcaacatgtaaagcctgtacccctgagcctgtgagcttgaaatcatgtctgtcc 120
Db 1670 GTGTGTGCAACATGTGAAGCCTGTACCCCTGAGCCTGTGAGCTTGAATCATGTCTGTC 1611

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OY 121 accacagggagacaagaattctctgaactgcaactctctaagaattgagagaaagccgttct 180
    |||
DB 1610 ACCACAGGGAGACAAGATTTCTGTAFACTGCACTCTCTAAGATTGGAGAGAAAACCTGTTT 1551
OY 181 accaagaagcttgaacatcctcctgagaaagaatgaagtgagactgtgttcaactcctg 240
    |||
DB 1550 ACCAAGAGACTTGAACATGCCCTCGAGAGAAATGAAGTGAAGTGAAGTGTGTTGTTACTCTTG 1491
OY 241 aaggagactcccaactgttgtctctcctctgcttaccatctgagagcaactctgcaagcgagaa 300
    |||
DB 1490 AAGGACCTTCCCACTGTGCTTCTCTGCTTCCATCATGAGACCATCTGCAAGCGGGA 1431
OY 301 aaccccaatgactgtgtctctcttcaaccccaaaattgttggagaaagccctagaaccctg 360
    |||
DB 1430 AACCCCATGATGATCTTGTGTCTTTCACCCAAATTTGTTGGAGAGACCTAGAAACCTTG 1371
OY 361 ccagaagaagtggtggtggaacaaagctccctgcaagaagcagccagctgcagagaaga 420
    |||
DB 1370 CCAGAGAAAGTGTGTGTGGAAACCAAGCTCCCTCGAAGACAGCCAGCTGCAGAGAAAG 1311
OY 421 ttccgcactctgagatcagagatattcggggaaccctcaaccccgcttcgggaagctg 480
    |||
DB 1310 TTCCCGCATCTGAGATTCAGAGATTTCCGGGAAACCTCAACACCGGCTTCGGAAGCTG 1251
OY 481 gacgagcagcaagagttcagttgcatcattccctgcaacaaagctgacctgcagcgagcgag 540
    |||
DB 1250 GACGAGACAGCAGAGATTCAGTGCATCATCTCTGCAACACCTGCTGCAGCCCATGGGC 1191
OY 541 tggcacaaccgggttggtgagacatcctgcacccctgaagaaatgcatgtatgctgtggtcag 600
    |||
DB 1190 TGGCAACAACCGGGTGGGCGAGATCTGCACCCCTGAGAGAAATGATGATGCTGTGGGCGAG 1131
OY 601 ggggcttggtggtgtggaagtgtgagagcaagagacaaactcttgatcgtgtgtgtgtg 660
    |||
DB 1130 GGGGCTTGTGGGCTGTGAAGTGTGAGGCCAAGCAGACACATCTTGTGAATGCTGTGGGCTGTG 1071
OY 661 ctgcagatcccgagactcgtctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 720
    |||
DB 1070 CTGCAGATCCGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
OY 721 gaaagagctgacgtgtgtcagtagccgtgcatcacagctatgaagaatggtggaactgtlac 780
    |||
DB 1010 GAAGGAGGCTGCAGTGTGCGAGTAGCCCTGCATACAGCTATGAAGCATGGGCAACTGTAC 951
OY 781 ctgactggagagagttctgaggtctagaaggtctagaagctacaaagaagaccatgagagct 840
    |||
DB 950 CTGACTGGAGAGTCTGAGAGTCTAGAGGCTCAGATAGCATACAGAGACATGACAGGCT 891
OY 841 accatcatgtccctcctcccaagcatgaagatgagccctgagagatgaccacagttgtgtgagc 900
    |||
DB 890 ACCATCATGTCCCTCCTGCCAGCATGAAGATGGCCCTGAGATGACCCACAGTTGTGTAGGC 831
OY 901 atcaatgctgtaacatttcaagagagggcccaaglttggtgtcccaagaacttgggcatcagc 960
    |||
DB 830 ATCACTGCTGTGAACATTCACAGAGGGGCCAGATTGCTGCCAGAACTTGGGCACTAGC 771
OY 961 ctggcacaactgtgtgtgagcaagaagagccaaaacaatcctgagatgttgaagcaattg 1020
    |||
DB 770 CTGGCAACTGTGTGTGTGAGCAAAAGAGCCAAACATCTTGATGTGTGACGGCAATGTG 711
OY 1021 aagcagtgcccataa 1035
    |||
DB 710 AAGCATGCCCATTTAA 696

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+ + 7g indy
Huan 1 2 1730 indy

```

DE PDGB DNA.
XX
KW Heme biosynthetic pathway; gene therapy; AIP; ALA;
KW delta-aminolevulinic acid; deficient porphyria; ADP;
KW porphyria cutanea tarda; PCT; hereditary coproporphyrin; HCP;
KW harderoporphyria; HDP; Variegata porphyria; VP;
KW congenital erythropoietic porphyria; CEP;
KW erythropoietic protoporphyria; EPP;
KW hepatoerythropoietic porphyria; HEP; ds.
XX
OS Homo sapiens.
XX
PN MO200107065-A2.
XX
PD 01-FEB-2001.
XX
XX
PF 27-JUL-2000; 2000WO-DK00425.
XX
PR 27-JUL-1999; 99DK-0001071.
XX
PR 19-APR-2000; 2000DK-0000667.
XX
PA (HEME-) HEMEBIOTECH AS.
XX
PI Gellerfors P, Fogh J;
XX
PI WPI; 2001-159639/16.
XX
PT Treatment or prevention of porphyria, by enzyme replacement or gene
PT therapy for correction of mutations, particularly in the
PT porphobilinogen deaminase gene
XX
PS Disclosure: Page 203-205; 207pp; English.
XX
XX
CC The present invention relates to treatment or prevention of a
CC disease caused by deficiency of at least one enzyme of the
CC heme biosynthetic pathway by administering at least one catalyst,
CC optionally combined with gene therapy of the relevant mutation.
CC The invention is useful for treating and/or preventing AIP, ALA
CC (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
CC cutanea tarda (PCT), hereditary coproporphyrin (HCP), harderoporphyria
CC (HDP), variegata porphyria (VP), congenital erythropoietic porphyria
CC (CEP), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
CC porphyria (HEP).
XX
SQ Sequence 3988 BP; 918 A; 1056 C; 1000 G; 1014 T; 0 other;

```

Query Match 100.0%; Score 1035; DB 22; Length 3988;
Best Local Similarity 100.0%; Pred. No. 3.7e-279;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 atgagagtgatctgcgtggtggtaccggaagagcaagctgtctgcatacagacgaagc 60
    |||
DB 1730 ATGAGAGTGTATGCGCGGTGTACCCGCAAGAGCAGCTTCTGCAATACAGAGGACAGT 1671
OY 61 gtgtggaacatgtgaagagctgtaccctcgtgagctcgaagtttgaatcatgtgtatgttc 120
    |||
DB 1670 GTGTGCAACATTTGAAGAGCTGTACCTGCTGAGTTTAAATCATTTGCTATGTCTC 1611
OY 121 accaagggagacaagaattcttgaactgcaactctctaagaattgagagaaagccgtgtt 180
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DB 1610 ACCACAGGGAGACAAGATTTCTGTAFACTGCACTCTCTAAGATTGGAGAGAAAACCTGTTT 1551
OY 181 accaagaagcttgaacatcctcctgagaaagaatgaagtgagactgtgttcaactcctg 240
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DB 1550 ACCAAGAGACTTGAACATGCCCTCGAGAGAAATGAAGTGAAGTGTGTTGTTACTCTTG 1491
OY 241 aaggagactcccaactgttgtctctcctctgcttaccatctgagagcaactctgcaagcgagaa 300
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DB 1490 AAGGACCTTCCCACTGTGCTTCTCTGCTTCCATCATGAGACCATCTGCAAGCGGGA 1431
OY 301 aaccccaatgactgtgtctctcttcaaccccaaaattgttggagaaagccctagaaccctg 360
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Db 1430 AACCTCATGATGCTCTTCTTTACCCAAATTTGTTGGAGAGACCTTAGAAMCCCTG 1371
Qy 361 ccagagaagaagtgtagtggaacacagctccctcgagaagacagccagctgagagaag 420
Db 1370 CCAGAGAAAGAGTGTGTGGGAACACACTCCCTGCGAAGAGCAGCCAGCTGCAAGAAAG 1311
Qy 421 tcccgacatcttgagtgtagtggaatctgggaaacctaacacccgagcttgagaatg 480
Db 1310 TTCCCTCATGATGATTCAGAGATTTCCGGGAACCTTCAACACCCGGCTTGGAAAGCTG 1251
Qy 481 gacagacagcagagatctcagtcacalcaccccgacacagctgagccctgacgacatg 540
Db 1250 GACGAGACACAGAGATGTAGTGCATCATCTGCGAAGAGCTGCGCTGAGGCGCATGGCC 1191
Qy 541 tggcacaacacgggttgaggagacatccctgacacccctgagaaatgcatgtagtgtag 600
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Qy 601 ggggacctggagtgtagtgtagtggaacacagacagacacacacacacacacacacac 660
Db 1130 GGGGCTTGGGCTGGAGATGCGACCCAAAGACAGACATCTGTGATCTGTGGGTGTG 1071
Qy 661 ctgcacagatcccgagacatctgctgctgacatcgctgaaaggacctctgagagacctg 720
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Qy 721 gaagagagctgagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtag 780
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Qy 781 ctgactgtagagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtg 840
Db 950 CTGACTGGAGAGTGTGAGATCTAGACGCTCAGATACATACAAAGACCATGACAGCT 891
Qy 841 accatccatctcccgacacagatgagctgagctgagctgagctgagctgagctgagctg 900
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Db 830 ATCACTGCTGCTGATTCACAGAGAGGCGCCAGTTGGCTGCCACAGATGAGATGAG 771
Qy 961 ctggcacaatctgctgtagcagaagagcgaacacatccctgagtgtagtgtagtgtag 1020
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Qy 1021 aacgagtgccatcaa 1035
Db 710 AACGATGCCCATTA 696

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RESULT 8
AX87632
ID AX87632 standard; cDNA; 1035 BP.
AC AX87632;
XX 26-Oct-1999 (first entry)

```

```

XX Human porphobilinogen deaminase clone 1.3.
XX

```

```

XX Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
XX porphyria cutanea tarda; hereditary coproporphyria;
XX haldroporphyria; congenital erythropoietic porphyria;
XX variegate porphyria; erythropoietic protoporphyria;
XX hepatoerythropoietic porphyria; acute intermittent porphyria;
XX gene therapy; enzyme replacement therapy; ds.
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XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX replace(513,A)
XX variation /*tag= a

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FT /note= "silent mutation"
FT replace(555,A)
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FT /note= "silent mutation"
FT replace(95,C)
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FT /note= "Asn to Phe substitution"
FT replace(1017,G)
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FT /note= "silent mutation"
FT replace(1018,C)
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FT /*tag= f
FT /note= "silent mutation"

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PM W09937325-A2.
PD 29-JUL-1999.
XX
PF 27-JAN-1999; 99WO-DK00040.
PR 30-DEC-1998; 98DK-0001748.
PR 27-JAN-1998; 98DK-0000112.
XX
PA (HEME-) HEMEBIOTEC AS.
PI Fogh J, Gellerfors P;
XX
DR WPI: 1999-478987/40.
XX

```

Treatment of acute intermittent porphyria and other porphyric diseases using an enzyme belonging to the haem biosynthetic pathway

Disclosure: Page 92; 100pp: English.

This is the nucleotide sequence of human PBGD clone 1.3 coding for an erythropoietic expressed form of porphobilinogen deaminase (PBGD). This enzyme catalyses the third, rate-limiting step of the haem biosynthetic pathway. PBGD was cloned from spleen, bone marrow, lymph node, lung, whole brain and adipose tissue cDNA using a nested PCR strategy. 8 PBGD clones were sequenced (see AX87630 and AX87632-38). Clone 1.3, from spleen cDNA, has 6 changes from the previously published sequence. Clone 1.1 (see AX87630) represents the most prevalent 'wild-type' allele in the population. Mutation of the PBGD gene is associated with the autosomal dominant disorder acute intermittent porphyria (AIP). A claimed method of treating a patient having a mutation in the PBGD gene comprises using a human PBGD cDNA sequence of either non-erythropoietic form (see AX87631) or erythropoietic form (especially clone 1.1 cDNA), according to the tissue in which PBGD should be expressed, and transfection of the patient with the relevant cDNA. Gene therapy treatment of CC patients with AIP by a correction of one of the specific point mutations identified as causing the disease by use of chimera-plasty gene repair is also claimed. Other enzymes involved in the haem biosynthetic pathway can also be used to treat various porphyrias.

Sequence 1035 BP; 250 A; 271 C; 303 G; 211 T; 0 other;

Query Match 99.88; Score 1033.4; DB 20; Length 1035; Best Local Similarity 99.9%; Pred. No. 5.7e-279; Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 atgagatgattcggtgggtacccgcaagagcagctgtcgcatacagaagagacgt 60
Db 1 atgagatgattcggtgggtacccgcaagagcagctgtcgcatacagaagagacgt 60
Qy 61 gtggtgcaacatgaaagcctgtaccctggcctgtagtgaatcatgctatgctc 120
Db 61 gtggtgcaacatgaaagcctgtaccctggcctgtagtgaatcatgctatgctc 120

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OY	121	accacaaaggagaaagatctctctgtatctgtacatctctctaagatttgggagaaagacctgttt	180
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OY	181	accaaagagctctgaacatctgcctcctggagaaatgaagatggagacctgtgtttccatctctg	240
Db	181	accaaagagagcttgaacatctgcctcctggagaaatgaagatggagacctgtgtttccatctctg	240
OY	241	aaagaaactctgccaactgtctctctctctctctctcaacatctgaaagccatctgcgaagcgaa	300
Db	241	aaagaaactctgccaactgtctctctctctctctctcaacatctgaaagccatctgcgaagcgaa	300
OY	301	aacccctaatgtatctgttctgtcttccccaataattgtttgggaaagacctgaagacctgt	360
Db	301	aacccctaatgtatctgttctgtcttccccaataattgtttgggaaagacctgaagacctgt	360
OY	361	ccaaagaaagagatctgt	420
Db	361	ccaaagaaagagatctgt	420
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OY	481	gaagcag	540
Db	481	gaagcag	540
OY	541	tggagacaaacccgggttgggagagatctctgcaccccttgaggaatgtatctgtctgtgtgtgt	600
Db	541	tggagacaaacccgggttgggagagatctctgcaccccttgaggaatgtatctgtctgtgtgtgt	600
OY	601	gggggcctctgggagctgt	660
Db	601	gggggcctctgggagctgt	660
OY	661	ctgcacgagatcccgagactctgtctgtctgtcatctgtgaagagggccttctctgtgagacctg	720
Db	661	ctgcacgagatcccgagactctgtctgtctgtcatctgtgaagagggccttctctgtgagacctg	720
OY	721	gaaggaagagctgtacgt	780
Db	721	gaaggaagagctgtacgt	780
OY	781	ctgcagcttgagagagctctgt	840
Db	781	ctgcagcttgagagagctctgt	840
OY	841	accatccaatctgtccctctgcgcagcagatgaagatgtgacctgtgaatgacccaacagttgtgtagc	900
Db	841	accatccaatctgtccctctgcgcagcagatgaagatgtgacctgtgaatgacccaacagttgtgtagc	900
OY	901	atacactgtctgtataacatcttccacgaggggccccagttgtgtgtgtgtgtgtgtgtgtgtgtgtgt	960
Db	901	atacactgtctgtataacatcttccacgaggggccccagttgtgtgtgtgtgtgtgtgtgtgtgtgtgt	960
OY	961	ctgcgcgaactgt	1020
Db	961	ctgcgcgaactgt	1020
OY	1021	aacgatgcccattaa	1035
Db	1021	aacgatgcccattaa	1035
RESULT	9		
AAx87633			
ID	AAx87633	standard; cDNA; 1035 BP.	
XX	AAx87633:		
DT	26-Oct-1999	(first entry)	
XX			

Accession	Gene	Protein	Enzyme	Substrate	Product	Reaction	Pathway	Reference
DE	Human porphobilinogen deaminase clone 2.1.							
XX								
KM	Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;							
KM	porphyria cutanea tarda; hereditary coproporphyria;							
KM	homoerythropoietic; congenital erythropoietic porphyria;							
KM	variegata porphyria; erythropoietic protoporphyria;							
KM	hepatoerythropoietic porphyria; acute intermittent porphyria;							
KM	gene therapy; enzyme replacement therapy; ds.							
XX								
OS	Homo sapiens.							
XX								
FH	Key	Location/Qualifiers						
FT	variation	replace(513,A)						
FT		/*tag- a						
FT		/note- "silent mutation"						
FT	variation	replace(555,A)						
FT		/*tag- b						
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FT	variation	replace(995,C)						
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FT		/note- "silent mutation"						
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FT		/*tag- e						
FT		/note- "silent mutation"						
FT	variation	replace(1020,T)						
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PN	MO9937325-A2.							
XX								
PD	29-JUL-1999.							
XX								
PF	27-JAN-1999;	99MO-DK00040.						
XX								
PR	30-DEC-1998;	98DK-0001748.						
PR	27-JAN-1998;	98DK-0000112.						
PA	(HEME-) HEMEBIOTEC AS.							
XX								
PI	Fogh J, Gellerfors P;							
XX								
DR	WPI: 1999-478987/40.							
XX								
PT	Treatment of acute intermittent porphyria and other porphyric							
PT	diseases using an enzyme belonging to the haem biosynthetic pathway							
XX								
PS	Disclosure: Page 92-93; 100pp; English.							
XX								
CC	This is the nucleotide sequence of human PBGD clone 2.1 coding for							
CC	an erythropoietic expressed form of porphobilinogen deaminase (PBGD).							
CC	This enzyme catalyses the third, rate-limiting step of the haem							
CC	biosynthetic pathway. PBGD was cloned from spleen, bone marrow,							
CC	lymph node, lung, whole brain and adipose tissue cDNA using a							
CC	nested PCR strategy. 8 PBGD clones were sequenced (see AA87630 and							
CC	AA87632-38). Clone 2.1, from bone marrow cDNA, has 6 changes from the							
CC	previously published sequence. Clone 1.1 (see AA87630) represents							
CC	the most prevalent 'wild-type' allele in the population. Mutation							
CC	of the PBGD gene is associated with the autosomal dominant disorder							
CC	acute intermittent porphyria (AIP). A claimed method of treating a							
CC	patient having a mutation in the PBGD gene comprises using a human							
CC	PBGD cDNA sequence of either non-erythropoietic form (see AA87631)							
CC	or erythropoietic form (especially clone 1.1 cDNA), according							
CC	to the tissue in which PBGD should be expressed, and transfection							
CC	of the patient with AIP by a correction of one of the specific point							
CC	mutations identified as causing the disease by use of chimeraplasty							
CC	gene repair is also claimed. Other enzymes involved in the haem							
CC	biosynthetic pathway can also be used to treat various porphyrias.							
XX								
XX	Sequence 1035 BP: 250 A; 271 C; 303 G; 211 T; 0 other;							

Query Match 99.8%; Score 1033.4; DB 20; Length 1035;
 Best Local Similarity 99.9%; Pred. No. 5,7e-279;
 Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 atgagagtgatcgcgtggtgtaaccgcgaagagccagctgtctgcatacagaagagacagt 60
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Oy 181 accaagagagcttgaacatctgcctctggagagaaagaaagtgagcctgtgttctcaactcttg 240
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Oy 481 gaagagagcagagagatctcagatctcagatctcagatctcagatctcagatctcagatctg 540
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Oy 901 atcacgtctcgttaacatctcagagagagccacagctgtgctgcacagaaactctggagacagc 960
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Oy 1021 aacgatgccattaa 1035
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 Db 1021 aacgatgccattaa 1035

RESULT 10
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 ID AAF72850 standard; DNA; 1035 BP.
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 AC AAF72850;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE PGGB from spleen.
 XX
 KW Heme biosynthetic pathway; gene therapy; AIP; ALA;
 KW delta-aminolevulinic acid; deficient porphyria; ADP;
 KW porphyria cutanea tarda; PCT; hereditary coproporphyrin; HCP;
 KW hereditary erythroid protoporphyria; HEP; VP;
 KW congenital erythropoietic porphyria; CEP;
 KW erythropoietic protoporphyria; EPP;
 KW hepatoerythropoietic porphyria; HEP; ds.
 XX
 OS Homo sapiens.
 OS
 PN MO200107065-A2.
 PD 01-FEB-2001.
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 PE 27-JUL-2000; 2000MO-DK00425.
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 PR 27-JUL-1999; 99DK-0001071.
 PR 19-APR-2000; 2000DK-0000667.
 XX
 PA (HEME-) HEMEBIOTECH AS.
 XX
 PI Gellerfors P, Fogh J;
 PI
 DR WPI; 2001-159639/16.
 XX
 PT Treatment or prevention of porphyria, by enzyme replacement or gene
 PT therapy for correction of mutations, particularly in the
 PT porphobilinogen deaminase gene -
 PS
 PS Disclosure; Page 200-201; 207pp; English.
 XX
 CC The present invention relates to treatment or prevention of a
 CC disease caused by deficiency of at least one enzyme of the
 CC heme biosynthetic pathway by administering at least one catalyst,
 CC optionally combined with gene therapy of the relevant mutation.
 CC The invention is useful for treating and/or preventing AIP, ALA
 CC (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
 CC cutanea tarda (PCT), hereditary coproporphyrin (HCP), hereditary
 CC (HDP), variegate porphyria (VP), congenital erythropoietic porphyria
 CC (CEP), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
 CC porphyria (HEP).
 XX
 SQ Sequence 1035 BP; 250 A; 271 C; 303 G; 211 T; 0 other;

Query Match 99.8%; Score 1033.4; DB 22; Length 1035;
 Best Local Similarity 99.9%; Pred. No. 5,7e-279;
 Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY	121	accacgaagggaagaatctctgttatctgtacatcctctcaagaagtctggagagaagaagcctgttt	180
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QY	181	accacaaaggagcttggaacatctgcccctggagagaagaatggagatggacctggtttctaacccctg	240
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QY	241	aaggaagacctgccaactgtgctctccctctctgaccttcacacatcggagaccatctgcgaagcgggaa	300
Db	241	aaggaagacctgccaactgtgctctccctctctgaccttcacacatcggagaccatctgcgaagcgggaa	300
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Db	301	aaccctcatatgtctgtctgtctcttcacacccaataattgtgtggagaagaacctgaagaacctgt	360
QY	361	ccaaagagaagaagttgtgtgtgggaacaacagctccctctcgagaagacagcccaagctgcagagaag	420
Db	361	ccaaagagaagaagttgtgtgtgggaacaacagctccctctcgagaagacagcccaagctgcagagaag	420
QY	421	ttcccgagatcttgagatcttcagaagatattctgaggagaaccccaacaccccgagcttcggagaagct	480
Db	421	ttcccgagatcttgagatcttcagaagatattctgaggagaaccccaacaccccgagcttcggagaagct	480
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Db	541	tggagacaacacccggagttctggagacgatactctgcacaaccccgagaagaatgcatagtctctggccag	600
QY	601	gggggcctctggagcgttgaggaagttgcagaccaaagacaagacacatcttgatctggctgggtgtg	660
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QY	661	ctgcagacgatacccgagactctgtctcgtcatctgactgcgaagagggcctctccctgagacactg	720
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QY	721	gaagaagagagctgcagttgcagctagccgctgcataacacgctcatgaagatctggacaactgtac	780
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QY	781	ctggaccttgagagagctctgagatcttagaagcgtctcagatagacataaagaagaacatctgcagct	840
Db	781	ctggaccttgagagagctctgagatcttagaagcgtctcagatagacataaagaagaacatctgcagct	840
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Db	841	accatcatatgtccctctgcgcagcatgaagaatgagccctcgagagatgacccaacagttgttaagc	900
QY	901	atcacctgctcgtlaaacattccaacgaagggccccaattgtgctgcgccagaacttgggcacacagc	960
Db	901	atcacctgctcgtlaaacattccaacgaagggccccaattgtgctgcgccagaacttgggcacacagc	960
QY	961	ctggcccaacatctgtgtcgtgcgaacgaagaaggcccaaaaacatcctgatatgttcacgcgaattg	1020
Db	961	ctggcccaacatctgtgtcgtgcgaacgaagaaggcccaaaaacatcctgatatgttcacgcgaattg	1020
QY	1021	aacgattgccattaa	1035
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ID	AAAF72851	standard; DNA: 1035 BP.	
XX	AAAF72851:		
XX			
DT	24-APR-2001	(first entry)	

Query Match	Best Local Similarity	Matches 1034; Conservative	Score 1033.4; DB 22; Length 1035;	Pred. No. 5.7e-279;	Mismatches 1; Indels 0; Gaps 0
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QY 181 accaagaagatctggaacaatctggaagaagaatgaagatgagctgtgttcaatccctcg 240					
DB 181 accaagaagatctggaacaatctggaagaagaatgaagatgagctgtgttcaatccctcg 240					
QY 241 aaggaacttcccaacttgtcttctcctctgcttcaacacatcggaagcattcgcgaagcgga 300					
DB 241 aaggaacttcccaacttgtcttctcctctgcttcaacacatcggaagcattcgcgaagcgga 300					
QY 301 aaacctcgaatgactgttcttcttccccaataattgtctggaagaagccctagaataacctg 360					
DE PDGs from bone marrow #1.					
XX Heme biosynthetic pathway; gene therapy; AIP; ALA;					
KM delta-aminolevulinic acid; deficient porphyria; ADP;					
KM porphyria cutanea tarda; PCT; hereditary coproporphyrin; HCP;					
KM harderoporphyria; HDP; variegata porphyria; VP;					
KM congenital erythropoietic porphyria; CEP;					
KM erythropoietic protoporphyria; EPP;					
KM hepatoerythropoietic porphyria; HEP; ds.					
XX Homo sapiens.					
PN WO200107065-A2.					
PD 01-FEB-2001.					
XX 27-JUL-2000; 2000WO-DK00425.					
PF 27-JUL-1999; 99DK-0001071.					
XX 19-APR-2000; 2000DK-0000667.					
PR (HEME-) HEMEBIOTECH AS.					
XX Gellerfors P, Fogh J;					
PI WPI; 2001-159639/16.					
XX Treatment or prevention of porphyria, by enzyme replacement or gene					
PT therapy for correction of mutations, particularly in the					
PT porphobilinogen deaminase gene -					
PS Disclosure; Page 201; 207pp; English.					
XX The present invention relates to treatment or prevention of a					
CC disease caused by deficiency of at least one enzyme of the					
CC heme biosynthetic pathway by administering at least one catalyst,					
CC optionally combined with gene therapy of the relevant mutation.					
CC The invention is useful for treating and/or preventing AIP, ALA					
CC (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria					
CC cutanea tarda (PCT), hereditary coproporphyrin (HCP), harderoporphyria					
CC (HDP), variegata porphyria (VP), congenital erythropoietic porphyria					
CC (CEP), erythropoietic protoporphyria (EPP) and hepatoerythropoietic					
CC porphyria (HEP).					
XX Sequence 1035 BP; 250 A; 271 C; 303 G; 211 T; 0 other;					

[illegible]

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FT		/note-"Asn to Thr substitution"
FT	variation	/replace(1017,G)
FT		/*tag- e
FT	variation	/note-"silent mutation"
FT		/replace(1018,C)
FT		/*tag- f
FT	variation	/note-"silent mutation"
FT		/replace(1020,T)
FT		/*tag- g
FT		/note-"silent mutation"
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PX	29-JUL-1999.	
PX	27-JAN-1999.	99WO-DK00040.
PX	30-DEC-1998.	98DK-0001748.
PR	27-JAN-1998;	98DB-0000112.
XX	(HEME-) HEMEBIOTECH AS.	
XX	Fogh J, Gellerfors P;	
PI	WPI: 1999-478987/40.	
DR	Treatment of acute intermittent porphyria and other porphyric diseases using an enzyme belonging to the haem biosynthetic pathway	
PT	Disclosure: Page 94; 100PP; English.	
PT	This is the nucleotide sequence of human PBGD clone 3.3 coding for an erythropoietic expressed form of uroporphobilogen deaminase (PBGD).	
CC	This enzyme catalyses the third, rate-limiting step of the haem biosynthetic pathway. PBGD was cloned from spleen, bone marrow, lymph node, lung, whole brain and adipose tissue cDNA using a nested PCR strategy. 8 PBGD clones were sequenced (see AAX87630 and AAX87632-38). Clone 3.3, from lymph node cDNA, has 6 changes from the previously published sequence. Clone 1.1 (see AAX87630) represents the most prevalent 'wild-type' allele in the population. Mutation of the PBGD gene is associated with the autosomal dominant disorder acute intermittent porphyria (AIP). A claimed method of treating a patient having a mutation in the PBGD gene comprises using a human PBGD cDNA sequence of either non-erythropoietic form (see AAX87631) or erythropoietic form (especially clone 1.1 cDNA), according to the tissue in which PBGD should be expressed, and transfection of the patient with the relevant cDNA. Gene therapy treatment of patients with AIP by a correction of one of the specific point mutations identified as causing the disease by use of chimeraplasty gene repair is also claimed. Other enzymes involved in the haem biosynthetic pathway can also be used to treat various porphyrias.	
CC	Sequence 1035 BP: 250 A; 270 C; 303 G; 212 T; 0 other:	
SO		
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Query Match 99.7% Score 1031.8; DB 20; Length 1035;		
Best Local Similarity 99.8%; Pred. No. 1.6e-278;		
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
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db	1 attgaagaagatcgcggttggttaccccgcaagaagcacagcttgtctcgcatacagaacggactt	60
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Db      61  gtgtgtgcaacatgaaagccctgcacccctgcagcttgtaaatcatgtctatgtcc 120
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Db      121  accacagggggaagaatcttgatctgactctctaagatgtggagaaaagcctgttt 180
Qy      181  accaagagcttgaaacatgaccttgagagaatgaatgaagtgagactgtgtttacccctg 240
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Qy      241  aagagacctgcccactgtgcttcctcctcctgcttcacacatcgagacatctgcaagcgga 300
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Qy      361  ccagagaaagtgtgtgtggaacacagctccctgcagaaagacgagccagctgcagagaaag 420
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Qy      481  gacgagcagcaggaatctcagctgcacatctcctgcagacagctgcgctcagcgcatgagc 540
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Qy      541  tggcacaacccggtgtgggcagatctctgcacccctggaggaatgatctatgctgtggcgag 600
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Qy      661  ctgcacgacatcccgaaacatctgctgtgcacatctgctgtgaaagggccttcctgagagcactg 720
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Qy      721  gaagagagctgcagctgtgcacatctgcagctgacacagctatgaagagatgtggcaactgtac 780
Db      721  gaagagagctgcagctgtgcacatctgcagctgacacagctatgaagagatgtggcaactgtac 780
Qy      781  ctgacttgagagagctgtgagctctagacggtcagatagacatacaagaagacatgcagagct 840
Db      781  ctgacttgagagagctgtgagctctagacggtcagatagacatacaagaagacatgcagagct 840
Qy      841  accatccatctgtccctgcgcccagatagaatgtgcctgtgagatgagaccacagctgtgtatgc 900
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Qy      901  atcactgtcgtcaaatctccacagagggcccccagttgtgtgcgccagaaacttgggcatacagc 960
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RESULT 13
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 AC AAF72854:

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XX      24-APR-2001 (first entry)
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XX      PDGB from lymph node #2.
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XX      Heme biosynthetic pathway; gene therapy; AIP; ALA;
Km      delta-aminolevulinic acid; deficient porphyria; ADP;
Km      porphyria cutanea tarda; PCT; hereditary coproporphyrin; HCP;
Km      harderoporphyria; HDP; variegata porphyria; VP;
Km      congenital erythropoietic porphyria; CEP;
Km      erythropoietic protoporphyria; EPP;
Km      hepatoerythropoietic porphyria; HEP; ds.
XX
XX      Homo sapiens.
OS
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XX      WO200107065-A2.
Pn
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Pd
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XX      27-JUL-2000; 2000WO-DK00425.
Pf
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XX      27-JUL-1999; 99DK-0001071.
Pr
XX      19-APR-2000; 2000DK-0000667.
XX
XX      (HEME-) HEMEBIOTECH AS.
Pa
XX
XX      Gellerfors P, Fogh J;
Pi
XX
XX      WPI: 2001-159639/16.
Dr
XX
XX      Treatment or prevention of porphyria, by enzyme replacement or gene
Pt      therapy for correction of mutations, particularly in the
Pp      porphobilinogen deaminase gene -
Pp      porphobilinogen deaminase gene -
Pp      porphobilinogen deaminase gene -
Ps
XX
XX      Disclosure; Page 202; 207pp; English.
Cc
XX
XX      The present invention relates to treatment or prevention of a
Cc      disease caused by deficiency of at least one enzyme of the
Cc      heme biosynthetic pathway by administering at least one catalyst,
Cc      optionally combined with gene therapy of the relevant mutation.
Cc      The invention is useful for treating and/or preventing AIP, ALA
Cc      (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
Cc      cutanea tarda (PCT), hereditary coproporphyrin (HCP), harderoporphyria
Cc      (HDP), variegata porphyria (VP), congenital erythropoietic porphyria
Cc      (CEP), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
Cc      porphyria (HEP).
Cc
XX
XX      Sequence 1035 BP; 250 A; 270 C; 303 G; 212 T; 0 other:
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Query Match 99.7%; Score 1031.8; DB 22; Length 1035;

Best Local Similarity 99.8%; Pred. No. 1.6e-276; Mismatches 2; Indels 0; Gaps 0;

Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      241  aagagacctgcccactgtgcttcctcctcctgcttcacacatcgagacatctgcaagcgga 300
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ID	AAx87638	standard; cDNA; 1035 BP.	
XX	AAx87638:		
XX			
DT	26-Oct-1999	(first entry)	
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XX	Human porphobilinogen deaminase clone 6.1.		
XX			
KM	Porphobilinogen deaminase: human; haem; ALA deficiency porphyria;		
KM	porphyria cutanea tarda; hereditary coproporphyria;		
KM	haldenporphyria; congenital erythropoietic porphyria;		
KM	variegata porphyria; erythropoietic protoporphyria;		
KM	hepatoerythropoietic porphyria; acute intermittent porphyria;		
KM	gene therapy; enzyme replacement therapy; ds.		
XX			
OS	Homo sapiens.		
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FT		/replace(995,C)
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FT	Variation	/note- "silent mutation"
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XX	27-JAN-1999:	99MO-DK00040.
PX		
PR	30-DEC-1998:	98DK-0001748.
XX	27-JAN-1998:	98DK-0000112.
PA	(HEME-) HEMEBIOTECH AS.	
PI		
PT	Fogh J, Gellerfors P;	
DR	WPI; 1999-478987/40.	
XX		
PS	Disclosure; Page 95; 100pp; English.	
CC	This is the nucleotide sequence of human PBGD clone 6.1 coding for	
CC	an erythropoietic expressed form of porphobilinogen deaminase (PBGD).	
CC	This enzyme catalyses the third, rate-limiting step of the haem	
CC	biosynthetic pathway. PBGD was cloned from spleen, bone marrow,	
CC	lymph node, lung, whole brain and adipose tissue cDNA using a	
CC	nested PCR strategy. 8 PBGD clones were sequenced (see AAX87630 and	
CC	AAX87632-38). Clone 6.1, from whole brain cDNA, has 8 changes from the	
CC	previously published sequence. Clone 1.1 (see AAX87630) represents	
CC	the most prevalent 'wild-type' allele in the population. Mutation	
CC	of the PBGD gene is associated with the autosomal dominant disorder	
CC	acute intermittent porphyria (AIP). A claimed method of treating a	
CC	patient having a mutation in the PBGD gene comprises using a human	
CC	PBGD cDNA sequence of either non-erythropoietic form (see AAX87631)	
CC	or erythropoietic form (especially clone 1.1 cDNA), according	
CC	to the tissue in which PBGD should be expressed, and transfection	
CC	of the patient with the relevant cDNA. Gene therapy treatment of	
CC	patients with AIP by a correction of one of the specific point	
CC	mutations identified as causing the disease by use of chimera-plasty	
CC	gene repair is also claimed. Other enzymes involved in the haem	
CC	biosynthetic pathway can also be used to treat various porphyrias.	
XX		
XQ	Sequence 1035 BP; 251 A; 272 C; 302 G; 210 T; 0 other;	

Query Match	99.5%	Score 1030.2;	DB 20;	Length 1035;
Best Local Similarity	99.7%	Pred. No. 4.5e-278;		
Matches 1032; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

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Db 301 aacctctcatgtatgtctgtcttcttcaaccnaaatltgttgtagaagaccctagaacacctg 360
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QY 1021 aacgattgccattaa 1035
Db 1021 aacgattgccattaa 1035

Search completed: October 6, 2001, 17:42:58
Job time: 305 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 18:32:02 ; Search time 2932.86 Seconds
(without alignments)
3869.903 Million cell updates/sec

Title: US-09-601-138-12
Perfect score: 1113
Sequence: 1 cacacagccactctccaag.....aattgaacgagtcacccatata 1113

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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97: gb_v50:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1113	100.0	1113	9	AX020193
2	1113	100.0	1113	10	AX079028
3	1106.6	99.4	1545	91	BC000520
4	1103.4	99.1	1377	93	HSPBDR2
5	1046	94.0	1380	93	HSPBDR
6	1035	93.0	1035	9	AX020182
7	1035	93.0	1035	10	AX079027
8	1035	93.0	1260	9	AX020191

9	1035	93.0	1260	10	AX079037	AX079037 Sequence
C 10	1035	93.0	3988	9	AX020190	AX020190 Sequence
C 11	1035	93.0	3988	10	AX079036	AX079036 Sequence
C 12	1033.4	92.8	1035	9	AX020183	AX020183 Sequence
C 13	1033.4	92.8	1035	9	AX020184	AX020184 Sequence
C 14	1033.4	92.8	1035	10	AX079029	AX079029 Sequence
C 15	1033.4	92.8	1035	10	AX079030	AX079030 Sequence
C 16	1032.6	92.8	5445	9	AX020192	AX020192 Sequence
C 17	1032.6	92.8	5446	10	AX079025	AX079025 Sequence
C 18	1031.8	92.7	1035	9	AX020187	AX020187 Sequence
C 19	1031.8	92.7	1035	10	AX079033	AX079033 Sequence
C 20	1030.2	92.6	1035	9	AX020189	AX020189 Sequence
C 21	1030.2	92.6	1035	10	AX079035	AX079035 Sequence
C 22	1028.6	92.4	1035	9	AX020186	AX020186 Sequence
C 23	1028.6	92.4	1035	10	AX079032	AX079032 Sequence
C 24	1021.4	91.8	1034	9	AX020185	AX020185 Sequence
C 25	1021.4	91.8	1034	9	AX020188	AX020188 Sequence
C 26	1021.4	91.8	1034	10	AX079031	AX079031 Sequence
C 27	1021.4	91.8	1034	10	AX079034	AX079034 Sequence
C 28	863.8	77.6	1571	94	BC003861	BC003861 Mus muscu
C 29	862	77.4	1086	95	RSPHEMC	Y12006 Rattus sp.
C 30	833.2	74.9	1412	95	RNPEGD	X06827 Rat (PBG-D)
C 31	797.6	71.7	1487	89	AK000628	AK000628 Homo sapi
C 32	236.2	21.2	122349	2	D90908	D90908 Synecocyst
C 33	176.8	15.9	9938	1	AE004938	AE004938 Pseudomon
C 34	173.6	15.6	6301	1	AE064061	AE064061 Pseudomon
C 35	172.2	15.5	10024	97	H0MPBGDA	M95623 Homo sapien
C 36	172.2	15.5	122459	84	HSAC000384	AC000384 Homo sapi
C 37	172.2	15.5	144794	82	AP001182	AP001182 Homo sapi
C 38	172.2	15.5	157405	82	AP001315	AP001315 Homo sapi
C 39	172.2	15.5	190762	82	AP000833	AP000833 Homo sapi
C 40	172.2	15.5	186511	82	AP000854	AP000854 Homo sapi
C 41	162.4	14.6	294250	2	AP001517	AP001517 Bacillus
C 42	162	14.6	110000	84	LMFCHR32-24	Confination (25 o
C 43	161	14.5	5852	2	AF221100	AF221100 Selenomon
C 44	160.6	14.4	269223	10	AX067466	AX067466 Sequence
C 45	159	14.3	1872	3	PSEHEMCD	M74844 Pseudomonas

ALIGNMENTS

RESULT 1	LOCUS	AX020193	1113 bp	DNA	PAT	07-SEP-2000
DEFINITION	Sequence 12 from Patent WO9337325.					
ACCESSION	AX020193					
VERSION	AX020193.1	GI:10043984				
KEYWORDS						
SOURCE	unidentified.					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 1113)					
AUTHORS	Fogh, J. and Gellerfors, P.					
TITLE	Method for treating acute intermittent porphyria (aip) and other porphyric diseases					
JOURNAL	Patient: WO 93/37325-A 12-29-JUL-1999;					
FEATURES	FOGH JENS (DK); HEHEBIOTEC A S (DK); GELLERFORS PAER (SE)					
source	1. 1113					
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BASE COUNT	274 a 294 c 323 g 222 t					
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Query Match 100.0%; Score 1113; DB 9; Length 1113;
Best Local Similarity 100.0%; Pred. No. 3.4e-256;
Matches 1113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 gaagaaacagcccaagatgaagtgatctgcgtggttacccgcaagagccagctgct 120
DB 61 GAAAGAAAACACCCAAAATGAGATGATGCGCGTGGGTACCCCAAGACGACCTTGCT 120
QY 121 gcgtacagagcagctggtggtggtggtggtggtggtggtggtggtggtggtggt 180
DB 121 GCCTACAG 180
QY 181 gaaatcattgtatgtatccacacaggggagacaaattcttgaatacctcctaagatt 240
DB 181 GAAATCATTTGCTATGTCACACAGGAGCAAGATTTGATTTGATGACCTCTTAAGATT 240
QY 241 ggaagaaagcagctgtttacacaaagagcttgaatacctcctggagaaatgaagtgagc 300
DB 241 GGAGAGAAAGCCCTTTTACCAAGAGCTTGAAATGCTCCCTGGAGAAAGATGAGTGC 300
QY 301 ctggtgttcacatctcttgaagagacccacacgtgtgtctctctctgtgtgtgtgtgt 360
DB 301 CTGTTGTTTCACTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 gcaatctgcaagcgagaaacccatgaatgctgtgtcttcttcaacaaattgttggg 420
DB 361 GCCATCTGCAAGCGGAGAAACCTCATGATGCTGTGCTTTCAACCAAAATTTGTTGG 420
QY 421 aagacccctagaagacccctgagagaaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
DB 421 AAGACCTAGAAACCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 gccagctgcaagaaagatcccgatctggaatgtcaggaatgtcggggaaacatcaac 540
DB 481 GCCAGCTGCGAGAGAAAGTTCCCGCATGCTGAGATTCAGAGATATTCGGGAAACCTCAAC 540
QY 541 acccgagcttggaagctgagcagagcagagagatgtcagatcattcattcctggcaacagct 600
DB 541 ACCGGCTTGGAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 ggcctgcaagcagatggtggtggtggtggtggtggtggtggtggtggtggtggtggt 660
DB 601 GGCTGCAAGGAG 660
QY 661 atgtatgctgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 720
DB 661 ATGTATCTGTGCGCCAGAGGAGGCTTGTGGGTGAGTGGAGAGAGAGAGAGAGAG 720
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DB 721 TTGATCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 780
QY 781 gcttctctgagcagcctggaagagcctgagtggtggtggtggtggtggtggtggtggt 840
DB 781 GCCTTCTGAGGACACCTGGAAGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAG 840
QY 841 aagagatggaacatgctgctgagcagagagagagagagagagagagagagagagagata 900
DB 841 AAGAGTGGCAACTGTACTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 900
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DB 961 GACCCACAGTTGTTAGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
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DB 1021 CAGAACTTGGGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 gatgttgcaagcgaatgtgaagatgtccattaa 1113
DB 1081 GATGTTGCAAGGCAATGTAAGAGATGCCATTAA 1113

RESULT	2
LOCUS	AX079028
DEFINITION	AX079028 1113 bp DNA PAT 22-FEB-2001 Sequence 4 from Patent WO0107065.
ACCESSION	AX079028
VERSION	AX079028.1 GI:13158603
KEYWORDS	.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1113) Gellerfors,P. and Fogh,J. Production of rhpbg and new therapeutic methods for treating patients with acute intermittent porphyria (aip) and other porphyric diseases Patent: WO 0107065-A 4 01-FEB-2001;
JOURNAL	Hembiotech A/S (DK)
FEATURES	Location/Qualifiers 1..1113 /organism="Homo sapiens" /db_xref="taxon:9606"
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BASE COUNT	274 a 294 c 323 g 222 t
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DB 181	GAAATCATTTGCTATGTGTCCACCAAGGGGCAAGATTCTGTATAGTGCATCTCTAAGATT	240		
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DB 241	GGAGAGAAAAGCCTGTATTCCAAAGGAGCTTGAACATGCCCTGGAGAAATGAAGTGCAC	300		
QY 301	cgtgtgttcatctctcttgaagaccgcccacatgtgcctccctccctggtctcaaccatcgga	360		
DB 301	CTGTGTGTTCATCTCTTGAAAGACCTGCCACAGCTCTCTCTCTGCTTCCACCATCGGA	360		
QY 361	ggcatctcgaaagcggaanaacctcatgtatgctgtgtcttccaccaaatattgttgg	420		
DB 361	GGCATCTGCAACGGGAAAAACCTCTATGATGCTGTCTTTCACCCAAAATTTGTTGGG	420		
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DB 481	GCCCACTCAGAGAAAGTTCCCGCATCTGTGGAGTTAGAGATTTGGGGAAAACCTCAAC	540		
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Db	601	GGCTGCGAGCGCCATGAGGCTGGCACAAACCGGGTTGGGACGATCCTGACACCTTGAGGAATGC	680
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OY	841	aagagttggagcacgttacctgtacctgtggaggagatcttggagttctaaagcagcctgaatagaata	900
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OY	901	caagagacacatgcagagcgtaccatccatltccctctgcccagcatgaagaatggccctgaagat	960
Db	901	CAGAGACCATGACAGGCTACCATCCATGATCCCTGCCGACGATGAAGTGGCCCTGAGGAT	960
OY	961	gaccacacagtttggtagagatcatcgtctctgttaaatctccagaagggccccagtttggctgcc	1020
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OY	1021	cagaactctgggcatcagcctgtggccaacttgttctgtgaagcaaggaagccaaaaacatctctg	1080
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LOCUS	BC000520
DEFINITION	BC000520 Homo sapiens, hydroxymethylbilane synthase, clone MGC:8561, mRNA, complete cds.
ACCESSION	BC000520
VERSION	BC000520.1 GI:12653496
KEYWORDS	MGC.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 1545)
TITLE	Strausberg,R.
JOURNAL	Direct Submission
REMARK	Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
COMMENT	NIH-MGC Project URL: http://mgc.ncl.nih.gov Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: DCTD/DTF CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/nisc_mgc@nigr.nih.gov Contact: nisc_mgc@nigr.nih.gov Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Benjamini,B., Blakesley,R.W., Bouffard,G.G., Brinkley,S., Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-T., Karlins,E., Legaspi,R., Lim,M., Maduro,Q.L., Mastello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stanculipop,S., Thomas,P.J., Tlionson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,E.D.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://Image.lnl.gov>
 Series: IRAL Plate: 1 Row: 3 Column: 24.

FEATURES

Location/Qualifiers

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CDS

BASE COUNT 380 a 433 c 443 g 309 t
 ORIGIN

Query Match

99.48; Score 1106.6; DB 91; Length 1545;
 Best Local Similarity 99.68; Pred. No. 1.1e-254;
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 QY 61 gaagaaacacgcccgaagatgagatgctcgcgtgggtacccgcaagacgaatgtct 120
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 DB 254 CGCATACAGACGACAGTGTGTGGCAACATTGAAGCCTGCTGACCTGCTGCACGTTT 313
 QY 181 gaatactgtctatgtccacacagggagacaagatctctatactgacatcttaagatc 240
 DB 314 GAATCATTTGCTATGTCACACAGGGGACAGATTTCTTATATCTGACCTCTAAGATT 373
 QY 241 gggagagaaagctgtcttaccaaagagcttgaacatgcctgtgaaagaaatgaatgagc 300
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 DB 434 CTGTTGTTTACTCTCTTGAAGACAGCTGCCACTGTGCTTCTCTGCTGCTCACCATCGCA 493
 QY 361 gcaatctgcaggggaaacacctcatgactgtgtgtctcttcaaccaaaatctgttgg 420
 DB 494 GCCATCTGCAAGCGGGAACCTCATGATGCTGTTGTCTTTCACCCAAATAATTTGTTGG 553
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RESULT 4

LOCUS HSPBGR2 1377 bp mRNA PRI 06-SEP-1995
 DEFINITION Human mRNA for non-erythropoietic porphobilinogen deaminase
 (hydroxymethylbilane synthase; EC4.3.1.8).
 ACCESSION X04808.1 GI:35308
 VERSION X04808.1 GI:35308
 KEYWORDS hydroxymethylbilane synthase; porphobilinogen deaminase.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1377)
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 Grandchamp, B., De Verneuil, H., Beaumont, C., Chretien, S., Walter, O.
 and Nordmann, Y.
 Tissue-specific expression of porphobilinogen deaminase. Two
 isoenzymes from a single gene
 Eur. J. Biochem. 162 (1), 105-110 (1987)
 COMMENT Data kindly reviewed (15-SEP-1987) by Grandchamp B.
 FEATURES

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1377

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BASE COUNT 327 a 367 c 391 g 292 t

ORIGIN

Query Match

99.1%; Score 1103.4; DB 93; Length 1377;

Best Local Similarity 99.5%; Pred. No. 6, 6e-254;

Matches 1107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 1081 GATGTTGCAGGCACTTAACGATGCCCATTTAA 1113

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RESULT 5

HSPBGR 1380 bp mRNA PRI 06-SEP-1995
DEFINITION Human mRNA for porphobilinogen deaminase (PBG-D, EC 4.3.1.8).
ACCESSION X04217
VERSION X04217.1 GI:35306
KEYWORDS deaminase; porphobilinogen deaminase.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1380)
AUTHORS Ratcliff N., Romeo P.H., Dubart A., Beaupain D., Cohen-Solal M. and
Goossens M.

TITLE Molecular cloning and complete primary sequence of human
erythrocyte porphobilinogen deaminase
JOURNAL Nucleic Acids Res. 14 (15), 5955-5968 (1986)
MEDLINE 86312872
COMMENT Porphobilinogen deaminase is the third enzyme of the heme
biosynthetic pathway. Deficiency of this enzyme leads to the
dominant hereditary disease Acute Intermittent Porphyria (AIP).

FEATURES

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Query Match

94.0%; Score 1046; DB 93; Length 1380;
Best Local Similarity 99.5%; Pred. No. 3, 7e-240;
Matches 1049; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Oy	360	agccatctgcgaagcgggagaaabccctcatgatactgtctgtctcttcaaccaaatgtgtg	419		
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LOCUS Sequence 3 from Patent WO0107065.
ACCESSION AX079027
VERSION AX079027.1 GI:13158602
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 1035)
AUTHORS Gellerfors, P. and Fogh, J.
TITLE Production of rhpbpd and new therapeutic methods for treating
patients with acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 0107065-A 3 01-FEB-2001;
Hembiotech A/S (DK)
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Query Match 93.0%; Score 1035; DB 10; Length 1035;
Best Local Similarity 100.0%; Pred. No. 1.7e-237;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Sequence 10 from Patent WO93937325.
ACCESSION AX020191
VERSION AX020191.1 GI:10043982
KEYWORDS
SOURCE
ORGANISM unidentified.
unclassified.
REFERENCE
1 (bases 1 to 1260)
AUTHORS Fogh, J. and Gellerfors, P.
TITLE Method for treating acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 93937325-A 10 29-JUL-1993;
FOGH JENS (DK); HEMBIOTECH A S (DK); GELLERFORS PAER (SE)
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 LOCUS
 DEFINITION Sequence 13 from Patent WO0107065.
 ACCESSION AX079037
 VERSION AX079037.1 GI:13158612
 KEYWORDS

SOURCE human.
 ORGANISM

Human sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1. (bases 1 to 1260)
 Gellerfors, P. and Fogh, J.
 Production of rnpbgd and new therapeutic methods for treating
 patients with acute intermittent porphyria (aip) and other
 porphyric diseases
 Patent: WO 0107065-A 13 01-FEB-2001.

JOURNAL

Hemebotech A/S (DK)

FEATURES

source Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 309 a 335 c 358 g 258 t
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Query Match 93.0%; Score 1035; DB 10; Length 1260;
 Best Local Similarity 100.0%; Pred. No. 1.6e-237;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	911	CTGACTGGAGAGAGTCTGTGAGTCTAGACGGCTCAGATACATACAAAGACCATGCAGGCT	970
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ACCESSION	AX020190		
VERSION	AX020190.1	GI:10043981	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
BASE COUNT	918 a	1056 c	1000 g
ORIGIN			

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KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Mammalia; Euteheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3988)
 AUTHORS Gellerfors, P. and Fogh, J.
 TITLE Production of rfbpd and new therapeutic methods for treating patients with acute intermittent porphyria (aip) and other porphyric diseases
 JOURNAL Patent: WO 0107065-A 12 01-FEB-2001;
 Hemeblotech A/S (DK)
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 1. 3988
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 /db_xref="taxon:9606"
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Query Match 93.0%; Score 1035; DB 10; Length 3988;
 Best Local Similarity 100.0%; Pred. No. 1.4e-237;
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 VERSION AX020183.1 GI:10043974
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 1035)
 AUTHORS Fogh, J. and Gellerfors, P.
 TITLE Method for treating acute intermittent porphyria (aip) and other porphyric diseases
 JOURNAL Patent: WO 9937325-A 2 29-JUL-1999;
 FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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 /db_xref="taxon:32644"

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 Db 61 gtgtgtgacaacatgaagcctgtaaccctgagctgagcttgaatcatctatgtcc 120
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Db 361 CCAGAGAAAGTGTGTGGGAACACAGCTCCCTGCGAAGACAGCCAGCTGCAGAAAG 420
Qy 499 tccccgcactgagctcagagatctggggaaccctcaaaccccggttcggaagctg 558
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RESULT 13
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DEFINITION AX020184
ACCESSION AX020184
VERSION AX020184.1 GI:10043975
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Fogh,J. and Gellerafors,P.
TITLE Method for treating acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 9937325-A 3 29-JUL-1999;
FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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Query Match 92.8%; Score 1033.4; DB 9; Length 1035;
Best Local Similarity 99.9%; Pred. No. 4e-237;
Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 79 atgagatgattcgcgtgtgtaacccgaagagcagctgtgctgcatacagcagacgt 138
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Qy 139 gtgtgtgacacatgaagaacccctgtaacccctgagctgcagctgtgaaatcatgtctatgctc 198
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Db 181 ACCAAGAGACTTGAACATTCCTCGAGAAAGATGAAGTGGACTGTGTTTCTACTTCCTTG 240
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Qy 379 aacctcatgatgctgtgtcttctcaaccaaattgtgtggagaagacctagaaaacctg 438
Db 301 AACCCCTCATGATGCTGTTCTCTTTCAACCAAAATTTGTTGGAGACAGCCCTTAACAAACCTG 360
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Db 421 TTCGCCATCTGAGATTTCAGAGATTATGGGGGAACCTCAACACCCGGCTTGGAAGCTG 480
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LOCUS Sequence 5 from Patent WO0107065.
ACCESSION AX079029
VERSION AX079029.1 GI:13158604
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Gellerfors, P. and Fogh, J.
TITLE Production of ribpgd and new therapeutic methods for treating patients with acute intermittent porphyria (aip) and other porphyric diseases
JOURNAL Patent: WO 0107065-A 5 01-FEB-2001;
Hembiotech A/S (DK)
FEATURES
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BASE COUNT 250 a 271 c 303 g 211 t
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Query Match 92.8%; Score 1033.4; DB 10; Length 1035;
Best Local Similarity 99.9%; Pred. No. 4e-237;
Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 79 atgagagtgatcgcgtggtgtaacccggaagccagctgtgctgatacaagagcagt 138
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VERSION AX079030.1 GI:13158605
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SOURCE Homo sapiens
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REFERENCE 1 (bases 1 to 1035)
AUTHORS Gellerfors, P. and Fogh, J.
TITLE Production of ribpgd and new therapeutic methods for treating patients with acute intermittent porphyria (aip) and other porphyric diseases
JOURNAL Patent: WO 0107065-A 6 01-FEB-2001;
Hembiotech A/S (DK)
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